

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:38:03 ; Search time 130.923 Seconds
(without alignments)
13025.213 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208
Perfect score: 30
Sequence: 1 catgtgttcaaccgttcgtctgttcca 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sv.*
12: gb_un.*
13: gb_vi.*
14: gb_brg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	30	6	AX224397	Sequence
2	30	100.0	255	6	AX224402	Sequence
3	30	100.0	1394	6	BD062176	Male tiss
4	30	100.0	1394	6	BD062177	Male tiss
5	30	100.0	1394	6	AX224394	Sequence
6	30	100.0	1394	6	AX224395	Sequence
7	30	100.0	3343	15	AF360356	Zea mays
8	24.2	80.7	158	6	AX224396	Sequence
9	22	73.3	1304	6	AX523502	Sequence
10	21.6	72.0	185503	9	AC151282	Continuation (212)
11	21.2	70.7	110000	15	AP008215	Continuation (286)
12	21.2	70.7	110000	15	AP008208	Continuation (322)
13	21.2	70.7	110000	15	AP008209	Continuation (207)
14	21.2	70.7	110000	15	AC091123	Continuation (207)
15	21.2	70.7	129778	15	AC091123	Continuation (207)
16	21.2	70.7	140723	15	AC091123	Continuation (207)
17	21.2	70.7	133675	14	AP006548	Oryza sat
18	21.2	70.7	155146	15	AP005710	Oryza sat
					AP004118	Oryza sat

19	21.2	70.7	158374	15	AP004786	Oryza sat
20	21.2	70.7	172058	15	AP003682	Oryza sat
21	21.2	70.7	178158	15	AC084320	Oryza sat
22	21	70.0	89829	15	AC119671	Oryza sat
23	21	70.0	93342	8	AC087245	Homo sapi
24	21	70.0	110000	14	AC153053	O
25	21	70.0	110000	15	AF008215	Oryza sat
26	21	70.0	110000	15	AF008216	Oryza sat
27	21	70.0	110000	15	AF008217	Oryza sat
28	21	70.0	110000	15	AF008217	Oryza sat
29	21	70.0	110000	15	AF008217	Oryza sat
30	21	70.0	110000	15	AF008217	Oryza sat
31	21	70.0	123472	15	AC120984	Oryza sat
32	21	70.0	143681	15	AC120984	Oryza sat
33	21	70.0	156394	14	AC026558	Oryza sat
34	21	70.0	158839	15	AC090882	Oryza sat
35	21	70.0	162198	15	AP005916	Oryza sat
36	21	70.0	187707	15	AC077693	Oryza sat
37	21	70.0	188854	9	AL626770	Mouse DNA
38	21	70.0	197160	15	AP005930	Oryza sat
39	21	70.0	253492	14	AC102160	Mus muscu
40	21	70.0	300029	15	AB017121	Oryza sat
41	21	70.0	345350	14	AC153038	Bos tauru
42	20.6	68.7	110000	15	AP008217	Oryza sat
43	20.6	68.7	169540	9	AC160062	Mus muscu
44	20.6	68.7	173088	15	AC109365	Oryza sat
45	20.6	68.7	196303	9	AC101349	Mus muscu

ALIGNMENTS

RESULT 1	AX224397	Sequence 4 from Patent WO0160997.	30 bp	DNA	linear	PAT 10-SEP-2001
LOCUS	AX224397	AX224397	GI:15554639			
DEFINITION	AX224397	AX224397	GI:15554639			
ACCESSION	AX224397	AX224397	GI:15554639			
VERSION	AX224397.1	AX224397.1	GI:15554639			
KEYWORDS	AX224397.1	AX224397.1	GI:15554639			
SOURCE	AX224397.1	AX224397.1	GI:15554639			
ORGANISM	AX224397.1	AX224397.1	GI:15554639			
REFERENCE	AX224397.1	AX224397.1	GI:15554639			
AUTHORS	AX224397.1	AX224397.1	GI:15554639			
TITLE	AX224397.1	AX224397.1	GI:15554639			
JOURNAL	AX224397.1	AX224397.1	GI:15554639			
FEATURES	AX224397.1	AX224397.1	GI:15554639			
source	AX224397.1	AX224397.1	GI:15554639			
location	AX224397.1	AX224397.1	GI:15554639			
organism	AX224397.1	AX224397.1	GI:15554639			
mol_type	AX224397.1	AX224397.1	GI:15554639			
db_xref	AX224397.1	AX224397.1	GI:15554639			

Query Match	AX224397	AX224397	GI:15554639			
Best Local Similarity	AX224397	AX224397	GI:15554639			
Matches	AX224397	AX224397	GI:15554639			
Conservative	AX224397	AX224397	GI:15554639			
Mismatches	AX224397	AX224397	GI:15554639			
Indels	AX224397	AX224397	GI:15554639			
Gaps	AX224397	AX224397	GI:15554639			
QY	AX224397	AX224397	GI:15554639			
DB	AX224397	AX224397	GI:15554639			
RESULT 2	AX224402	AX224402	GI:15554644			
LOCUS	AX224402	AX224402	GI:15554644			
DEFINITION	AX224402	AX224402	GI:15554644			
ACCESSION	AX224402	AX224402	GI:15554644			
VERSION	AX224402.1	AX224402.1	GI:15554644			
KEYWORDS	AX224402	AX224402	GI:15554644			
SOURCE	AX224402	AX224402	GI:15554644			

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ORGANISM      Zea mays
DEFINITION    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ACCESSION    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
VERSION      clade; Panicoideae; Andropogoneae; Zea.
KEYWORDS     1
SOURCE       Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
ORGANISM     Male tissue-preferred regulatory region and method of using same
TITLE        Patent: WO 0160997-A 9 23-AUG-2001;
JOURNAL      PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES     Location/Qualifiers
             1..255
             /organism="Zea mays"
             /mol_type="unassigned DNA"
             /db_xref="taxon:4577"
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 39 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 68

RESULT 3
LOCUS      BD062176                1394 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Male tissue-preferred regulatory region and method of using same.
ACCESSION  BD062176
VERSION    BD062176.1 GI:22607781
KEYWORDS   JP 2001520523-A/1.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
           1 (bases 1 to 1394)
REFERENCE  1
AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall,T.L.
TITLE     Male tissue-preferred regulatory region and method of using same
JOURNAL   PIONEER HI BRED INTERNATIONAL INC
COMMENT   PN JP 2001520523-A/1
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,
PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FEATURES     source
             1..1394
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 30
Db 1179 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 1208

RESULT 5
LOCUS      AX224394                1394 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION Sequence 1 from Patent WO0160997.
ACCESSION  AX224394
VERSION    AX224394.1 GI:155554636
KEYWORDS   Zea mays
SOURCE     Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
           1
REFERENCE  1
AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE     Male tissue-preferred regulatory region and method of using same
JOURNAL   PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES     Location/Qualifiers
             1..1394
             /organism="Zea mays"
             /mol_type="unassigned DNA"
             /db_xref="taxon:4577"
ORIGIN
Query Match      100.0%; Score 30; DB 6; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 30
Db 1179 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 1208

RESULT 4
LOCUS      BD062177                1394 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Male tissue-preferred regulatory region and method of using same.
ACCESSION  BD062177
VERSION    BD062177.1 GI:22607782
KEYWORDS   JP 2001520523-A/2.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
           1 (bases 1 to 1394)
REFERENCE  1
AUTHORS   Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall,T.L.
TITLE     Male tissue-preferred regulatory region and method of using same
JOURNAL   PIONEER HI BRED INTERNATIONAL INC
COMMENT   PN JP 2001520523-A/2
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,
PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FEATURES     source
             1..1394
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
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Query Match      100.0%; Score 30; DB 6; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 30
Db 1179 CATGCTTGTTCACCGTTCGTCCTGTGTTCCA 1208

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Db 1179 CATGCTGTTCACACCGTTCGCTTGTTC 1208

RESULT 6
LOCUS AX224395
DEFINITION Sequence 2 from Patent WO0160997.
ACCESSION AX224395
VERSION AX224395.1 GI:15554637
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Albertsen, M.C., Fox, T.W., Garmaat, C.W., Huffman, G. and Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 2 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers
source 1. .1394
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACACCGTTCGCTTGTTC 30
Db 1179 CATGCTGTTCACACCGTTCGCTTGTTC 1208

RESULT 7

LOCUS AF360356
DEFINITION Zea mays male fertility protein (Ms45) gene, complete cds.
ACCESSION AF360356
VERSION AF360356.1 GI:14028756
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Fox, T.W., Trimmell, M.R. and Albertsen, M.C.
TITLE Cloning of Ms45, a gene required for male fertility from Zea mays
JOURNAL Unpublished
REFERENCES 1. (bases 1 to 3343)
2. (bases 1 to 3343)

AUTHORS Fox, T.W., Trimmell, M.R. and Albertsen, M.C.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
FEATURES Location/Qualifiers
source 1. .3343
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
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/gene="Ms45"

gene
mRNA
CDS

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SRKQHLNILEGEGTGRLLRYPETSGVYVVLKGLVFPNGVQISEDHQFLFSETTNC
RIMYVLEGFRAGEVEFANLPGFPDYNVSRNGRQGFVAIDCCTPAQEVFAKRPMLR
TLYKFLSLKVLTKAARMHTVLLALDGEGRVVEVLEDRGHEVWKLVSVEVGRK
LWIGTVAHHIATIPYLED"

ORIGIN

Query Match 100.0%; Score 30; DB 15; Length 3343;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACACCGTTCGCTTGTTC 30
Db 1179 CATGCTGTTCACACCGTTCGCTTGTTC 1208

RESULT 8

LOCUS AX224396
DEFINITION Sequence 3 from Patent WO0160997.
ACCESSION AX224396
VERSION AX224396.1 GI:15554638
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Albertsen, M.C., Fox, T.W., Garmaat, C.W., Huffman, G. and Kendall, T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 3 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers
source 1. .158
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"

ORIGIN

Query Match 80.7%; Score 24.2; DB 6; Length 158;
Best Local Similarity 89.7%; Pred. No. 9.1;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACACCGTTCGCTTGTTC 29
Db 25 CATGCTGTTCACACCGTTCGCTTGTTC 53

RESULT 9

LOCUS AX523502/c
DEFINITION Sequence 90 from Patent WO02064788.
ACCESSION AX523502
VERSION AX523502.1 GI:24412398
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02064788-A 90 22-AUG-2002;

Diadexus, Inc. (US)
 Location/Qualifiers
 1. .1304
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source

ORIGIN

Query Match 73.3%; Score 22; DB 6; Length 1304;
 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACACCGTTCGTCGTGTTCCA 30
 Db 1155 CTTTCTGTTCCTCCCGTTCCTCTGTTCCA 1126

RESULT 10
 AC151282/c
 LOCUS
 DEFINITION Mus musculus BAC clone RP23-461H1 from chromosome 17, complete sequence.

ACCESSION AC151282 AC124638
 VERSION AC151282.3 GI:71533339
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Tomlinson, C. and Cotton, M.
 TITLE The sequence of Mus musculus BAC clone RP23-461H1
 JOURNAL Unpublished (2001)
 REFERENCE
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (24-AUG-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-2005) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT
 On Jul 30, 2005 this sequence version replaced gi:57544825.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: submissions@wustl.edu

----- Summary Statistics
 Center project name: M_BA0461H01
 Drafting center: WIBR

NOTICE:
 This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.
 This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence

complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.
 If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:
 The BAC Library has been constructed by Kazutoyo Oseegawa and Minako Tatenno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

This sequence is the entire insert of the clone.

FEATURES
 source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="17"
 /clone="RP23-461H1"
 /clone_lib="RPCI-23"
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 /note="Sequence derived from PCR product of project DNA"
 unsure 36165..36266
 /note="Sequence derived from one plasmid subclone."
 unsure 37190..37291
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 unsure 37612..37642
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 unsure 38054..38103
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 misc_feature 38247..38458
 /note="Sequence derived from PCR product of project DNA"
 unsure 38459..38760
 /note="Unresolved simple sequence repeat."
 unsure 40259..40297
 /note="Sequence derived from one plasmid subclone."
 unsure 40341..40404
 /note="Sequence derived from one plasmid subclone."
 unsure 42926..43056
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 /note="Sequence derived from PCR product of genomic DNA"
 misc_feature 95577..95635
 /note="Sequence derived from PCR product of project DNA"
 unsure 99723..100104
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 unsure 151397..151697
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ORIGIN
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 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 ATGCTTGTTCACACCGTTCGTCGTGTTCC 29
 Db 47380 ATGCTTGTTCACACCGTTCGTCGTGTTCC 47353

RESULT 11
 AP008215.211
 WPCOMMENT

Sequence split into 227 fragments LOCUS AP008215 Accession AP008215

Fragment Name	Begin	End
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AP008215_001	100001	210000
AP008215_002	200001	310000
AP008215_003	300001	410000
AP008215_004	400001	510000
AP008215_005	500001	610000
AP008215_006	600001	710000
AP008215_007	700001	810000
AP008215_008	800001	910000
AP008215_009	900001	1010000
AP008215_010	1000001	1110000
AP008215_011	1100001	1210000
AP008215_012	1200001	1310000
AP008215_013	1300001	1410000
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AP008215_015	1500001	1610000
AP008215_016	1600001	1710000
AP008215_017	1700001	1810000
AP008215_018	1800001	1910000
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AP008215_037	3700001	3810000
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AP008215_039	3900001	4010000
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AP008215_043	4300001	4410000
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AP008215_079	7900001	8010000
AP008215_080	8000001	8110000
AP008215_081	8100001	8210000
AP008215_082	8200001	8310000
AP008215_083	8300001	8410000
AP008215_084	8400001	8510000
AP008215_085	8500001	8610000
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AP008215_191 19100001 19210000
AP008215_192 19200001 19310000
AP008215_193 19300001 19410000
AP008215_194 19400001 19510000
AP008215_195 19500001 19610000
AP008215_196 19600001 19710000

Query Match 70.7%; Score 21.2; DB 15; Length 110000;
Best Local Similarity 88.5%; Fred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGTGTTAACCGTTCGTGTTGTTCCA 30
Db 84254 CATGTTTAACCGTTCGTGTTATTTCCA 84279

RESULT 12
AP008208_285
WPCOMMENT
Sequence split into 360 fragments LOCUS AP008208 Accession AP008208
Fragment Name Begin End
AP008208_000 1 110000
AP008208_001 100001 210000
AP008208_002 200001 310000
AP008208_003 300001 410000
AP008208_004 400001 510000
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AP008208_007 700001 810000
AP008208_008 800001 910000
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AP008208_010 1000001 1110000
AP008208_011 1100001 1210000
AP008208_012 1200001 1310000
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AP008208_014 1400001 1510000
AP008208_015 1500001 1610000
AP008208_016 1600001 1710000
AP008208_017 1700001 1810000
AP008208_018 1800001 1910000
AP008208_019 1900001 2010000
AP008208_020 2000001 2110000
AP008208_021 2100001 2210000
AP008208_022 2200001 2310000
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AP008208_191 19100001 19210000
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AP008208_196 19600001 19710000

Query Match 70.74; Score 21.2; DB 15; Length 110000;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Cy 5 CTGTTCAACCGTTCGTCCTTATCCA 30
Db 29637 CATGTTAACCGTTCGTCCTTATCCA 29662

RESULT 13
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AP008209_004 400001 510000
AP008209_005 500001 610000
AP008209_006 600001 710000
AP008209_007 700001 810000
AP008209_008 800001 910000
AP008209_009 900001 1010000
AP008209_010 1000001 1110000
AP008209_011 1100001 1210000

AP008209_012	1200001	1310000	AP008209_085	8500001	8610000
AP008209_013	1300001	1410000	AP008209_086	8600001	8710000
AP008209_014	1400001	1510000	AP008209_087	8700001	8810000
AP008209_015	1500001	1610000	AP008209_088	8800001	8910000
AP008209_016	1600001	1710000	AP008209_089	8900001	9010000
AP008209_017	1700001	1810000	AP008209_090	9000001	9110000
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AP008209_019	1900001	2010000	AP008209_092	9200001	9310000
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AP008209_021	2100001	2210000	AP008209_094	9400001	9510000
AP008209_022	2200001	2310000	AP008209_095	9500001	9610000
AP008209_023	2300001	2410000	AP008209_096	9600001	9710000
AP008209_024	2400001	2510000	AP008209_097	9700001	9810000
AP008209_025	2500001	2610000	AP008209_098	9800001	9910000
AP008209_026	2600001	2710000	AP008209_099	9900001	10010000
AP008209_027	2700001	2810000	AP008209_100	10000001	10110000
AP008209_028	2800001	2910000	AP008209_101	10100001	10210000
AP008209_029	2900001	3010000	AP008209_102	10200001	10310000
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AP008209_045	4500001	4610000	AP008209_118	11800001	11910000
AP008209_046	4600001	4710000	AP008209_119	11900001	12010000
AP008209_047	4700001	4810000	AP008209_120	12000001	12110000
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AP008209_076	7600001	7710000	AP008209_149	14900001	15010000
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AP008209_081	8100001	8210000	AP008209_154	15400001	15510000
AP008209_082	8200001	8310000	AP008209_155	15500001	15610000
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AP008209_084	8400001	8510000	AP008209_157	15700001	15810000

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Query Match 70.7%; Score 21.2; DB 15; Length 110000;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGTTCACCGTTCGTCCTGTGTTCCA 30

Db 59888 CAGTTTACCGTTCGTCCTGTGTTCAA 59863

RESULT 15
AC091123/c 129778 bp DNA linear PLN 09-AUG-2001
LOCUS AC091123
DEFINITION Oryza sativa chromosome 3 BAC OSJNB0093E13 genomic sequence,
complete sequence.
ACCESSION AC091123.4 GI:14670090
VERSION AC091123.4
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 129778)
AUTHORS Buell, C.R., Yuan, Q., Qiyang, S., Moffat, K.S., Hill, J.N.,
Gansberger, K., Brenner, M., Burgess, S., Hance, M., Shvartsbeyn, M.,
Tsitrin, T., Riggs, P., Hsiao, J., Zismann, V., Blunt, S., Pai, G.,
VanAken, S.E., Utterback, T.R., Feldblyum, T.V., Quackenbush, J.,
Salzberg, S.L., White, O. and Fraser, C.M.
Oryza sativa chromosome 3 BAC OSJNB0093E13 genomic sequence
Unpublished
2 (bases 1 to 129778)
REFERENCE Buell, R.
AUTHORS Direct Submission
TITLE Submitted (31-MAR-2001) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 129778)
REFERENCE Buell, R.
AUTHORS Direct Submission
TITLE Submitted (11-JUL-2001) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr, Rockville, MD 20850, USA


```

/translation="MEDWVVLGSGDGSVELHDGSDVGGSDTESFVQVVRGAAD
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GICEENPDDIEIFDEEESDDEEDIGSSDLETDSDEYIEESTDEESDYEEEDITDLES
SDDEEDTSSHDEDDDDDDSLDDGSECDFEEDKIGTENPDDESVDVTGSSDDEE
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DFFYGDLYDIETESSCEECERVCVCGRCMELIDGEEFYQLITGDEFQGTQLGEIIG
GDASGADDEEFPDAGESDHTADAGDGEAHGDSADMGNSAAAABPASTSSQFOQ
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VGVDVASNTAAAFPLDTLALQDGVVSLAVFYLLFGVYVYLLLRICALN"
repeat_region      18749..18856
                    /rpt_family="(GGA)n"
repeat_region      complement(20115..20185)
                    /rpt_family="AT_rich"
gene               21519..21947
                    /gene="OSJNBb0093E13.8"
                    /note="predicted by fgenesh"
mRNA               <21519..>21947
                    /gene="OSJNBb0093E13.8"
CDS                21519..21947
                    /gene="OSJNBb0093E13.8"
                    /codon_start=1
                    /product="hypothetical protein"

Query Match       70.7%; Score 21.2; DB 15; Length 129778;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5  CTTGTTCAACCGTTCGTTCTGTTCCA 30
Db      20209 CATGTTAACCGTTCGTTCTGTTCAA 20184

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Search completed: March 5, 2006, 21:55:36
 Job time : 135.048 secs

GenCore version 5.1.7
Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 19.9642 Seconds
(without alignments)
10014.946 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208

Perfect score: 30

Sequence: 1 catgctgttcaaccgtctgtctgtccca 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*

1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2001ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*
14: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	5	AAH76335
2	30	100.0	255	5	AAH76340
3	30	100.0	1394	2	AAH76340
4	30	100.0	1394	2	AAH76340
5	30	100.0	1394	2	AAH76332
6	30	100.0	1394	5	AAH76332
7	24.2	80.7	158	5	AAH76334
8	22	73.3	1304	6	AAH76334
9	20.4	68.0	1542	6	AAH76334
10	20.2	67.3	2357	6	AAH76334
11	20	66.7	2000	11	AAH76334
12	20	66.7	2000	11	AAH76334
13	20	66.7	2000	11	AAH76334
14	19.6	65.3	1735	11	AAH76334
15	19.6	65.3	2000	8	AAH76334
16	19.6	65.3	2000	8	AAH76334
17	19.6	65.3	2000	8	AAH76334
18	19.6	65.3	2000	8	AAH76334
19	19.6	65.3	2000	11	AAH76334

C	20	19.6	65.3	2000	12	ADJ40977
	21	19.4	64.7	2240	2	AAH7668
	22	19.4	64.7	2243	4	AAH7668
	23	19.4	64.7	2243	9	AAH7668
	24	19.4	64.7	34980	6	ABQ81845
	25	19.2	64.0	2000	8	ADAY1777
	26	19	63.3	1324	3	ADAY1777
	27	19	63.3	1388	3	AAH76335
	28	19	63.3	1821	10	ADH93879
	29	19	63.3	2000	11	ADH93879
	30	19	63.3	5671	4	AAH76335
	31	19	63.3	5671	5	AAH76335
	32	19	63.3	5671	5	AAH76335
	33	19	63.3	5671	9	ADH32792
	34	19	63.3	198522	11	ACN44010
	35	18.8	62.7	883	6	ABK65288
	36	18.8	62.7	883	10	ADD30938
	37	18.8	62.7	883	10	ADD30938
	38	18.8	62.7	883	12	ADI41918
	39	18.8	62.7	1083	4	AAH76335
	40	18.8	62.7	1083	8	AAH76335
	41	18.8	62.7	1893	10	AAH76335
	42	18.8	62.7	1902	4	AAH76335
	43	18.8	62.7	1902	8	AAH76335
	44	18.8	62.7	1908	12	ADH63835
	45	18.8	62.7	2000	11	ADH63835

ALIGNMENTS

RESULT 1

AAH76335

ID AAH76335 standard; DNA; 30 BP.

AC AAH76335;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 male tissue-preferred regulatory region fragment.

MS45; male tissue; regulatory region; transcription; male fertility;

KW hybrid seed; ds.

OS Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US004527.

PR 15-FEB-2000; 2000US-00504487.

PA (PION-) PIONEER HI-BRED INT INC.

PI Albertsen MC, Fox TW, Garnaat CW, Huifman G, Kendall TL;

DR WPI; 2001-514772/56.

PT A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

PS Claim 5; Page 47; 50pp; English.

CC The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (i) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

```
CC present sequence represents a DNA fragment -152 to -181 bases upstream of
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
CC nucleotide sequence
XX
SQ Sequence 30 BP; 4 A; 9 C; 5 G; 12 T; 0 U; 0 Other;

Query Match      100.0%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
   |||||
Db 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30

RESULT 2
AAH76340
ID AAH76340 standard; DNA; 255 BP.
XX
AC AAH76340;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter fragment.
XX
KW Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; promoter; ds.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US004527.
XX
PR 15-FEB-2000; 2000US-00504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX
DR WPI; 2001-514772/56.
XX
CC A male tissue-preferred regulatory region comprising nucleotide sequences
CC essential for initiating transcription of the MS45 gene useful for
CC mediating fertility in a male plant.
XX
PS Example 5; Fig 8; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the MS45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a Z. mays Ms45 promoter fragment
XX
SQ Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;

Query Match      100.0%; Score 30; DB 5; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
   |||||
Db 39 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 68

RESULT 3
AAH7408
ID AAH7408 standard; DNA; 1394 BP.
XX
```

```
XX
AC AAH7408;
XX
DT 08-JUN-1999 (first entry)
XX
DE Zea mays Ms45 male tissue-preferred regulatory region.
XX
KW Ms45; male; tissue-preferred; regulatory region; plant cells;
KW plant tissue; differentiated; maize; hybrid seed; fertility; ss.
XX
OS Zea mays.
XX
PN WO9859061-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US012895.
XX
PR 23-JUN-1997; 97US-00880499.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;
XX
DR WPI; 1999-105628/09.
XX
CC New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
CC - useful in mediating plant fertility, especially hybrid seed production.
XX
PS Claim 2; Page 22-23; 39pp; English.
XX
CC The sequence is that encoding an Ms45 male tissue-preferred regulatory
CC region. It may be used in the construction of a vector for a method of
CC producing exogenous genes in a male tissue- preferred manner, which is
CC useful in restoring or conferring fertility, such as in hybrid seed
CC production. In conferring fertility, a monocot/dicot plant is transformed
CC with the exogenous nucleotide sequence (a male sterility gene, preferably
CC Ms45), which encodes a product selected from auxins, rolB and dietheria
CC toxin. Hybrid seeds are produced by cross-pollinating maize male fertile
CC and infertile plants
XX
SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;

Query Match      100.0%; Score 30; DB 2; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 30
   |||||
Db 1179 CATGCTTGTTCACACCGTTCGTCCTGTGTTCCA 1208

RESULT 4
AAH7409
ID AAH7409 standard; DNA; 1394 BP.
XX
AC AAH7409;
XX
DT 08-JUN-1999 (first entry)
XX
DE Zea mays Ms45 male tissue-preferred regulatory region.
XX
KW Ms45; male; tissue-preferred; regulatory region; plant cells;
KW plant tissue; differentiated; hybrid seed; fertility; ss.
XX
OS Zea mays.
XX
PN WO9859061-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US012895.
XX
```


PN	XX	WO200264788-A2.
PD	XX	22-AUG-2002.
XX	XX	
PF	XX	20-NOV-2001; 2001WO-US045080.
XX	XX	
PR	XX	20-NOV-2000; 2000US-0252054P.
XX	XX	
PA	XX	(DIAD-) DIADEXUS INC.
XX	XX	
PI	XX	Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX	XX	
DR	XX	WPI; 2002-657601/70.
XX	XX	
PT	XX	New lung specific nucleic acid useful in gene therapy or as vaccines for
PT	XX	treating lung cancer (e.g. squamous cell carcinoma) or non-carcinoma lung
PT	XX	diseases, as well as for diagnosing, monitoring or staging these
PT	XX	diseases.
XX	XX	
PS	XX	Claim 1; Page 206; 282pp; English.
XX	XX	
CC	XX	The present invention describes an isolated lung specific nucleic acid
CC	XX	(LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid
CC	XX	sequences comprising 17 - 733 amino acids, given in ABP52873 to ABP52965;
CC	XX	(b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp);
CC	XX	(c) given in ABQ75262 to ABQ75376; (c) selectively hybridizes to (a) or (b);
CC	XX	or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific
CC	XX	protein (LSP) sequences have cytostatic activity and can be used in gene
CC	XX	therapy and vaccines. LSNA and LSPs are useful for diagnosing and
CC	XX	monitoring the presence and metastases of lung cancer in a patient. An
CC	XX	antibody that specifically binds to an LSP can be used for determining
CC	XX	the presence of an LSP in a sample, as well as for treating a patient
CC	XX	with lung cancer, particularly by inducing an immune response against the
CC	XX	lung cancer cell expressing the LSNA or LSPs. In particular, these LSNA
CC	XX	and LSPs are useful for identifying, diagnosing, monitoring, staging,
CC	XX	imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-
CC	XX	cancerous disease states in lung
XX	XX	
SQ	XX	Sequence 1304 BP; 352 A; 347 C; 314 G; 291 T; 0 U; 0 Other;
		Query Match 73.3%; Score 22; DB 6; Length 1304;
		Best Local Similarity 83.3%; Pred. No. 18;
		Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0
QY	1	CATGCTTGTTCACCGTTCGTCTGTGTC 30
DB	1155	CTTCTTGTTCCTCCGTTCTTGTGTC 1126
		RESULT 9
ABZ13819		ID ABZ13819 standard; DNA; 1542 BP.
XX	XX	ABZ13819;
AC	XX	
DT	XX	21-JAN-2003 (first entry)
XX	XX	
DE	XX	Arabidopsis thaliana stress regulated gene SEQ ID NO 1624.
XX	XX	
KW	XX	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX	XX	
OS	XX	Arabidopsis thaliana.
PN	XX	WO200216655-A2.
XX	XX	
PD	XX	28-FEB-2002.
XX	XX	
PF	XX	24-AUG-2001; 2001WO-US026685.
XX	XX	
PR	XX	24-AUG-2000; 2000US-0227866P.
PR	XX	26-JAN-2001; 2001US-0264647P.
PR	XX	22-JUN-2001; 2001US-0300111P.
XX	XX	

PA (SCRI) SCRIPPS RES INST.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 DR
 XX Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 XX Claim 144; SEQ ID NO 1624; 577bp + Sequence Listing; English.
 PS
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office.
 XX
 XX Sequence 1542 BP; 345 A; 382 C; 370 G; 445 T; 0 U; 0 Other;
 SQ
 Query Match 68.0%; Score 20.4; DB 6; Length 1542;
 Best Local Similarity 80.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 CAGCTGTGTCACCGTTCGTCGTTTCCA 30
 Db 237 CAGTATGTTTCACCAATCGTCGTTTCCA 266

RESULT 10
 ID ACA44013 standard; DNA; 2397 BP.
 AC ACA44013;
 AC

19-JUN-2003 (first entry)
 DE Prokaryotic essential gene #25670.
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 OS Pseudomonas putida.
 SN WO200277183-A2.
 SN 03-OCT-2002.
 XX

21-MAR-2002; 2002WO-US009107;
 XX 21-MAR-2001; 2001US-00815242.
 XX 06-SEP-2001; 2001US-00948993.
 XX 25-OCT-2001; 2001US-0342923P.
 XX 08-FEB-2002; 2002US-00072851.
 XX 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu RH;
 PI WPI; 2003-029926/02.
 DR P-FSDB; ABU40143.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 14; SEQ ID NO 31883; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2397 BP; 415 A; 825 C; 781 G; 376 T; 0 U; 0 Other;
 Query Match 67.3%; Score 20.2; DB 8; Length 2397;
 Best Local Similarity 86.0%; Pred. No. 1.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CAGCTGTGTCACCGTTCGTCGTTG 25
 Db 516 CAGCTGTGTCACCGTTCGTCGTTG 540

RESULT 11
 ID ACL37526 standard; cDNA; 2000 BP.
 AC ACL37526;
 AC
 XX 02-JUN-2005 (first entry)
 XX Rice stress-regulated promoter SEQ ID NO:16089.
 DE ss; abiotic stress tolerance; transgenic plant; plant; cereal;
 XX agriculture.
 KW Oryza sativa.
 SN WO2003008540-A2.
 SN 30-JAN-2003.
 XX 21-JUN-2002; 2002WO-US019668.
 XX 22-JUN-2001; 2001US-0300112P.
 XX 24-AUG-2001; 2001US-0314662P.
 XX 26-SEP-2001; 2001US-0325277P.
 XX 21-NOV-2001; 2001US-0332132P.
 XX

```

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 16089; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 2000 BP; 607 A; 443 C; 399 G; 549 T; 0 U; 2 Other;

Query Match 66.7%; Score 20; DB 11; Length 2000;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGTCCTGTTCCTCA 30
Db 1576 TGCATGTTGACCGTTCGTCCTATTCA 1603

RESULT 12
ACL34976
ID ACL34976 standard; cDNA; 2000 BP.
XX
XX ACL34976;
AC
XX 02-JUN-2005 (first entry)
DT
XX Rice stress-regulated promoter SEQ ID NO:13539.
DE
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
XX
XX Oryza sativa.
OS
XX WO2003008540-A2.
PN
XX 30-JAN-2003.
PD
XX 21-JUN-2002; 2002WO-US019668.
PF
XX 22-JUN-2001; 2001US-0300112P.
PR
XX 24-AUG-2001; 2001US-0314662P.
PR
XX 26-SEP-2001; 2001US-0325277P.
PR
XX 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 13539; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 2000 BP; 552 A; 438 C; 444 G; 566 T; 0 U; 0 Other;

Query Match 66.7%; Score 20; DB 11; Length 2000;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGTCCTGTTCCTCA 30
Db 1179 TACATGTTTAAACCGTTCGTCCTATTCA 1206

RESULT 13
ADJ40785
ID ADJ40785 standard; cDNA; 2000 BP.
XX
XX ADJ40785;
AC
XX 06-MAY-2004 (first entry)
DT
XX Plant cDNA #1785.
DE
XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KW antifungal.
XX
XX Eukaryota.
OS
XX US2004016025-A1.
PN
XX 22-JAN-2004.
PD
XX 26-SEP-2002; 2002US-00260238.
PF
XX 26-SEP-2001; 2001US-0325277P.
PR
XX 26-SEP-2001; 2001US-0325448P.
PR
XX 04-APR-2002; 2002US-0370620P.
XX
XX (BUDW/) BUDWORTH P.
PA
XX (MOUG/) MOUGHAMER T.
PA
XX (BRIG/) BRIGGS S P.
PA
XX (COOP/) COOPER B.
PA
XX (GLAZ/) GLAZEBROOK J.
PA
XX (GOFF/) GOFF S A.
PA
XX (KATA/) KATAGIRI F.
PA
XX (KEP/) KREPS J.
PA
XX (PROV/) PROVART N.
PA
XX (RICK/) RICKE D.
PA
XX (ZHUT/) ZHU T.
XX
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI

```

PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX WPI; 2004-190374/18.
XX New rice promoter, useful for manipulating crop plants to alter or
XX improve phenotypic characteristics, e.g. produce large quantities of oil
XX or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX or high nutritional value.

PS Claim 26, SEQ ID NO 1785; 230pp; English.

CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 2000 BP; 552 A; 438 C; 444 G; 566 T; 0 U; 0 Other;

Query Match 66.7%; Score 20; DB 12; Length 2000;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TGCTTGTCAACCGTTCGTCGTGTTCCA 30

DB 1179 TACATGTTTAAACCGTTCGTCGTATTATCA 1206

RESULT 14

ACL35519
ID ACL35519 standard; cDNA; 1735 BP.

AC ACL35519;

DT 02-JUN-2005 (first entry)

DE Rice stress-regulated promoter SEQ ID NO:14082.

XX as; abiotic stress tolerance, transgenic plant; plant; cereal;
XX agriculture.

OS Oryza sativa.

XX WO2003008540-A2.

XX 30-JAN-2003.

XX 21-JUN-2002; 2002WO-US019668.

XX 22-JUN-2001; 2001US-0300112P.

XX 24-AUG-2001; 2001US-0314662P.

XX 26-SEP-2001; 2001US-0325277P.

XX 21-NOV-2001; 2001US-0332132P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
XX Moughamer T, Provart N, Ricke D, Zhu T;

XX WPI; 2003-248011/24.

XX New stress-responsive nucleic acid, useful for altering the
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX stress, salt stress or osmotic stress.

PS Claim 48; SEQ ID NO 14082; 89pp; English.

CC The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention

XX SQ Sequence 1735 BP; 502 A; 368 C; 279 G; 581 T; 0 U; 5 Other;

Query Match 65.3%; Score 19.6; DB 11; Length 1735;
Best Local Similarity 84.6%; Pred. No. 2e+02;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CTCTGTTCAACCGTTCGTCGTGTTCCA 30

DB 394 CATGTTTAAACCGTTCGTCGTATTATCA 419

RESULT 15

ADAY2061

ID ADAY2061 standard; DNA; 2000 BP.

AC ADAY2061;

DT 20-NOV-2003 (first entry)

DE Rice gene, SEQ ID 5386.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
XX Gene; ds.

OS Oryza sativa.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to

XX PT pathogenic infection for conferring resistance or tolerance to a plant to
XX PT bacterial, fungal or viral infection by determining or detecting plant
XX PT gene expression.

XX Claim 27; SEQ ID NO 5386; 89pp; English.

XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX
SQ Sequence 2000 BP; 605 A; 377 C; 326 G; 590 T; 0 U; 2 Other;

Query Match 65.3%; Score 19.6; DB 8; Length 2000;
Best Local Similarity 84.6%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CTTGTTCAACCGTTCGTTCTTCTTCCA 30
| ||||| ||||| ||||| |||||
Db 974 CATGTTTAAACCGTTCGTTCTTCTTCAA 999

Search completed: March 5, 2006, 18:11:38
Job time : 22.9642 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 18:11:59 / Search time 141.632 Seconds
(without alignments)
9910.279 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208

Perfect score: 30
Sequence: 1 catgctgttcaaccgttctgttcca 30

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30	100.0	687	9	CC656939 OGMDQ20TV
C 2	30	100.0	915	10	CG224225 OG1AG08TV
C 3	30	100.0	963	9	CC656939
C 4	27.4	91.3	296	10	CG700474 ZMBB001f1
C 5	22.2	74.0	534	5	BU035739
C 6	21.2	70.7	626	5	BU030489 OHJ7N19.Y
C 7	21.2	70.7	792	7	CN137013 OX1 54.E0
C 8	21.2	70.7	792	7	CN137013
C 9	21	70.0	154	1	AA811551
C 10	21	70.0	351	11	CR192459 Reverse s
C 11	21	70.0	571	11	CR064270 Reverse s
C 12	21	70.0	599	11	CR233964 Reverse s
C 13	21	70.0	769	11	CR188179 Reverse s
C 14	21	70.0	835	9	CC848693
C 15	21	70.0	835	9	CC860012
C 16	20.6	69.3	586	7	CO853973
C 17	20.6	68.7	412	8	R12648
C 18	20.6	68.7	450	8	R12618
C 19	20.6	68.7	582	1	AU290776
C 20	20.6	68.7	594	8	DR437963
C 21	20.6	68.7	681	9	AZ817790
C 22	20.6	68.7	1144	9	CC271930 CH261-112

23	20.4	68.0	353	9	AQ61553
24	20.4	68.0	373	3	BP857382
25	20.4	68.0	396	2	BE522930
26	20.4	68.0	398	3	BP836596
27	20.4	68.0	514	2	BP354154
28	20.4	68.0	515	3	BP561510
29	20.4	68.0	536	1	AV439701
30	20.4	68.0	559	1	AV825937
C 31	20.4	68.0	590	6	CA230882
C 32	20.4	68.0	590	7	CV153842
C 33	20.4	68.0	598	10	CW788317
C 34	20.4	68.0	602	10	CL583422
C 35	20.4	68.0	603	9	BZ694195
C 36	20.4	68.0	615	9	AQ453944
C 37	20.4	68.0	639	7	CV153844
C 38	20.4	68.0	668	9	AQ260121
C 39	20.4	68.0	779	6	CD825116
C 40	20.4	68.0	807	6	CD836362
C 41	20.4	68.0	835	9	BH480110
C 42	20.4	68.0	967	9	BZ684538
C 43	20.4	68.0	1205	9	BI0570
C 44	20.4	68.0	431	8	R32995
C 45	20.2	67.3			

ALIGNMENTS

RESULT 1
LOCUS CC656939 687 bp DNA linear GSS 19-JUN-2003
DEFINITION OGMDQ20TV ZM.0.7.1.5 KB Zea mays genomic clone ZMMBMA0554D15,
genomic survey sequence.
ACCESSION CC656939
VERSION CC656939.1 GI:32060231
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 687)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGMDQ20TV
Contact: Cathy Whitelaw
TIGR

7912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. 687
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0554D15"
/notes="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

Query Match 100.0%; Score 30; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. NO. 0.024;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGTGTTCAACCGTTCGCTTGTTCCA 30

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Db      397 CATGCTGTTCAACCGTTCGTCTGTGTTCCA 368
|||||
RESULT 2
CG224225          CG224225          915 bp      DNA      linear      GSS 22-AUG-2003
LOCUS             OGIAG08TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0716B15,
DEFINITION        genomic survey sequence.
ACCESSION         CG224225
VERSION           CG224225.1 GI:34124113
KEYWORDS          GSS.
SOURCE            Zea mays
ORGANISM          Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS           Whitelaw C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
                  Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
                  Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
TITLE             Consortium for Maize Genomics
JOURNAL           Unpublished (2002)
COMMENT           Other GSSs: OGIAG08TV
                  Contact: Cathy Whitelaw
                  TIGR
                  9712 Medical Center Drive, Rockville, MD 20850, USA
                  Tel: 301-838-5843
                  Fax: 301-838-0208
                  Email: whitelaw@tigr.org
                  Seq primer: TF
                  Class: methylation filtered.
                  Location/Qualifiers
                    1..915
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /strain="B73"
                    /db_xref="taxon:4577"
                    /clone_lib="ZMMBMA0716B15"
                    /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                    methylation filtered genomic DNA library"

FEATURES
source
Query Match      100.0%; Score 30; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATGCTGTTCAACCGTTCGTCTGTGTTCCA 30
|||||
Db      776 CATGCTGTTCAACCGTTCGTCTGTGTTCCA 805
|||||

RESULT 4
CW445575
LOCUS             CW445575
DEFINITION        296 bp      DNA      linear      GSS 02-NOV-2004
                  fbb001f170m16k0 Sorghum methylation filtered library (LibID: 104)
                  Sorghum bicolor genomic clone fbb001f170m16, genomic survey
                  sequence.
ACCESSION         CW445575
VERSION           CW445575.1 GI:55193536
KEYWORDS          GSS.
SOURCE            Sorghum bicolor (sorghum)
ORGANISM          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                  clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
AUTHORS           Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
                  Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
                  McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,
                  Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddelloh, J.A. and
                  Martienssen, R.A.
TITLE             Sorghum genome sequencing by methylation filtration
JOURNAL           PLOS Biol. 3 (1), e13 (2005)
PUBMED            15660154
COMMENT           Contact: Bedell JA
                  Orion Genomics, LLC
                  4041 Forest Park Ave, St. Louis, MO 63108, USA
                  Tel: 314 615 6979
                  Fax: 314 615 5975
                  Email: jbedell@oriongenomics.com
                  Plate: fbb001f170 row: m column: 16
                  Seq primer: k Reverse
                  Class: methylation filtered
                  High quality sequence stop: 296.
                  Location/Qualifiers
                    1..296
                    /organism="Sorghum bicolor"
                    /mol_type="genomic DNA"
                    /cultivar="ATx623"
                    /db_xref="taxon:4558"
                    /clone="fbb001f170m16"
                    /clone_lib="Sorghum methylation filtered library (LibID:
                    104)"
                    /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
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FEATURES
source
Query Match      100.0%; Score 30; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATGCTGTTCAACCGTTCGTCTGTGTTCCA 30
|||||
Db      558 CATGCTGTTCAACCGTTCGTCTGTGTTCCA 587
|||||

RESULT 3
CC656933
LOCUS             CC656933
DEFINITION        OGW2020TM_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0554D15,
                  genomic survey sequence.
ACCESSION         CC656933
VERSION           CC656933.1 GI:32060225
KEYWORDS          GSS.
SOURCE            Zea mays
ORGANISM          Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS           Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
                  Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
                  Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
TITLE             Consortium for Maize Genomics
JOURNAL           Unpublished (2002)
COMMENT           Other_GSSs: OGW2020TV

```

end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSK(-) vector and electroporated into *E. coli* cells. This is a methylation filtered library."

ORIGIN

Query Match 91.3%; Score 27.4; DB 10; Length 296;
Best Local Similarity 96.8%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 1;
Qy 2 ATGCTGTTCACCGTTCGTCCTTCCCA 30
|||||
Db 140 ATGCTGTTCACCGTTCGTCCTTCCCA 168

RESULT 5

CG700474/c
LOCUS
DEFINITION ZMMB00174H15f ZMMB0c (EcoRI) Zea mays genomic clone ZMMB0c0174H15
5', genomic survey sequence.
CG700474
ACCESSION
VERSION CG700474.1 GI:37688275
KEYWORDS
SOURCE GSS.
ORGANISM Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 308)
Bharti A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zobovetz, V., Fuke, G., Yu, R., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)

TITLE

Contact: Bharti, A.K.

JOURNAL

Dr. Joachim Messing's lab

COMMENT

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 57.

FEATURES

source

1..308
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMB0c0174H15"
/lab_host="E. coli DH10B"
/clone_lib="ZMMB0c (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 74.0%; Score 22.2; DB 10; Length 308;
Best Local Similarity 88.9%; Pred. No. 60;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGTCCTTCTT 27
|||||

Db 226 CATGCTGTTCACCGTTCGTCCTTCTT 200
|||||

RESULT 6

BU035739/c
LOCUS
DEFINITION BU035739 534 bp mRNA linear EST 23-AUG-2002
clone QHJ7N19, mRNA sequence.
ACCESSION
VERSION BU035739.1 GI:22471259
KEYWORDS

ORIGIN

1..534
Location/Qualifiers
/organism="Helianthus annuus"
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/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="QHJ7N19"
/lab_host="E. coli"
/note="Vector: pBSGDNASf1AB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformationally made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUE-flowers environmental stress
TAG LIB-QH EFGHJ sunflower RHA280
TAG_SEQ-CGAATGCGG3"

SOURCE

ORGANISM Helianthus annuus (common sunflower)

Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

REFERENCE

AUTHORS

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/

TITLE

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Ammundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3046, see http://cgpdb.ucdavis.edu/
for details.

Plate: QHJ7 row: N column: 19.
Location/Qualifiers
1..534
/organism="Helianthus annuus"
/mol_type="mRNA"
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/clone="QHJ7N19"
/lab_host="E. coli"
/note="Vector: pBSGDNASf1AB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformationally made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUE-flowers environmental stress
TAG LIB-QH EFGHJ sunflower RHA280
TAG_SEQ-CGAATGCGG3"

FEATURES

source

1..534
Location/Qualifiers
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="QHJ7N19"
/lab_host="E. coli"
/note="Vector: pBSGDNASf1AB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformationally made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUE-flowers environmental stress
TAG LIB-QH EFGHJ sunflower RHA280
TAG_SEQ-CGAATGCGG3"

ORIGIN

Query Match 70.7%; Score 21.2; DB 5; Length 534;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ATGCTGTTCACCGTTCGTCCTTCTT 27
|||||

Db 104 ATGCTGTTCACCGTTCGTCCTTCTT 79
|||||

RESULT 7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

EST.

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

EST.

BU030489
QHJ15120.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
clone QHJ15120, mRNA sequence.

626 bp

EST.

GI:22466009

Helianthus annuus (common sunflower)

Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

1 (bases 1 to 626)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compenomics.ucdavis.edu/>
 Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Amundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.org [michelmore@vegmil.ucdavis.edu]
 belongs to contig QH_CA_Contig3046, see <http://cgdb.ucdavis.edu/>
 for details.
 Plate: QHJ15 row: I column: 20.

FEATURES

Location/Qualifiers
 1..626
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="RHA280"
 /db_xref="taxon:4232"
 /clones="QHJ15120"
 /lab_hosts="E.coli"
 /clone_lib="OH_EFGHJ sunflower RHA280"
 /note="Vector: pRCDNASfiAB: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
 TAG TISSUE=flowers environmental stress
 TAG LIB=OH_EFGHJ sunflower RHA280
 TAG_SEQ=CGAATCGGG"

ORIGIN

Query Match 70.7%; Score 21.2; DB 5; Length 626;
 Best Local Similarity 88.5%; Pred. No. 1.9e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ATGCTTCTCAACGTTGCTGCTGTT 27
 |||||
 Db 104 ATGCTTCTCAACGTTGCTGCTGTT 79
 |||||

RESULT 8
 CN137013
 LOCUS
 DEFINITION
 OX1_54_E01.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone OX1_54_E01_A002 5', mRNA sequence.
 ACCESSION
 CN137013
 VERSION
 CN137013.1 GI:45970259
 EST.
 Sorghum bicolor (sorghum)
 Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 792)
 Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
 An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
 Other ESTs: OX1_54_E01.b1.A002
 Contact: Cordonnier-Pratt, M.M.
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics; University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
 Seq primer: Sug5 (CTTCTGCTCTAAAGCTGGC).

FEATURES

Location/Qualifiers
 1..792
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /clone="OX1_54_E01_A002"
 /lab_hosts="DH10B-TI phage-resistant E. coli"
 /clone_lib="Oxidatively-stressed leaves and roots"
 /note="Organ: Leaf and Root; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned and unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Query Match 70.7%; Score 21.2; DB 7; Length 792;
 Best Local Similarity 88.5%; Pred. No. 1.9e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTGTTCACACGTTGCTGTTGTTCCA 30
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 Db 17 CTCTCCACCGTTGCTGTTCTTCCA 42
 |||||

RESULT 9

AA811551/c
 LOCUS
 DEFINITION
 Oa99a03.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1320412 3', similar to SW:COPE_BOVIN_Q28104 COATOMER EPSILON SUBUNIT ;, mRNA sequence.
 ACCESSION
 AA811551
 VERSION
 AA811551.1 GI:2881162
 EST.
 Homo sapiens (human)
 Homo sapiens
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 154)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-@email.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
 Trace considered overall poor quality

Insert Length: 1232 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amerham
High quality sequence stop: 1.
Location/Qualifiers
1. 154

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1320412"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP CCB1"
/note="Vector; p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAAGTCGAGCGCCGCTCATTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 154;
Best Local Similarity 82.8%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGCTGTTCCTCA 30
DB 43 AAGCTTTGTAACCCATCGCTGTTCCTCA 15

RESULT 10

CR192459/c

LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN146a06, genomic survey sequence.
DEFINITION
ACCESSION CR192459
VERSION
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 351)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

Location/Qualifiers

1. 351
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN146a06"
/clone_lib="MHPN"

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 351;
Best Local Similarity 82.8%; Pred. No. 2.1e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGCTGTTCCTCA 30
DB 307 ATGCTGTTCACCGTTCGCTGTTCCTCA 279

RESULT 11

CR064270/c

LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN190119, genomic survey sequence.
DEFINITION
ACCESSION CR064270
VERSION
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 571)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

Location/Qualifiers

1. 571
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN190119"
/clone_lib="MHPN"

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 571;
Best Local Similarity 82.8%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGCTGTTCCTCA 30
DB 309 ATGCTGTTCACCGTTCGCTGTTCCTCA 281

RESULT 12

CR233964/c

LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN144h08, genomic survey sequence.
DEFINITION
ACCESSION CR233964
VERSION
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 599)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

Location/Qualifiers

1. 599
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN144h08"
/clone_lib="MHPN"

ORIGIN

Query Match 70.0%; Score 21; DB 1; Length 599;
Best Local Similarity 82.8%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCACCGTTCGCTGTTCCTCA 30

Wed Mar 8 14:16:28 2006

us-10-713-381-1_copy_1179_1208.rst

Page 7

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:54:12 ; Search time 8.38752 Seconds
(without alignments)
6357.883 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208

Perfect score: 30

Sequence: 1.catgctgttcaaccgtctgttccca 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:**

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:**
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:**
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:**
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq:**
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:**
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:**
- 9: /cgn2_6/ptodata/1/ina/backfileseq1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	1394	3	US-08-880-499-1
2	30	100.0	1394	3	US-08-880-499-2
3	19.4	64.7	2243	2	US-07-937-609-15
4	19.4	64.7	2243	3	US-08-029-170-15
5	19.4	64.7	2243	3	US-09-443-745-15
6	19	63.3	45571	3	US-09-949-016-16262
7	18.8	62.7	7812	3	US-09-368-590-1
8	18.8	62.7	8756	3	US-09-949-016-1438
9	18.8	62.7	112874	3	US-08-961-527-132
10	18.8	62.7	112874	3	US-09-949-016-13180
11	18.6	62.0	549	3	US-09-270-767-29480
12	18.6	62.0	1120	3	US-09-270-767-13492
13	18.4	61.3	1260	3	US-09-248-796A-3293
14	18.2	60.7	2710	3	US-09-573-080A-7
15	18	60.0	601	3	US-09-949-016-200252
16	18	60.0	601	3	US-09-949-016-200253
17	18	60.0	889	3	US-08-956-171E-1190
18	18	60.0	889	3	US-08-781-986A-1190
19	18	60.0	1591	2	US-08-728-956-3
20	18	60.0	33675	3	US-09-921-992-2
21	18	60.0	111509	3	US-09-949-016-17379
22	18	60.0	254366	3	US-09-822-871-3
23	17.8	59.3	393	3	US-09-563-110-1388
24	17.8	59.3	393	3	US-09-107-433-743

ALIGNMENTS

RESULT 1
US-08-880-499-1
; Sequence 1, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Huffman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-1

Query Match 100.0%; Score 30; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 0.0012; Indels 0; Gaps 0; Matches 30; Conservative 0; Mismatches 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCGTGTCCA 30
Db 1179 CATGCTTGTTCAACCGTTCGTCGTGTCCA 1208

RESULT 2
US-08-880-499-2
; Sequence 2, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Carl, Garmaat W.
; APPLICANT: Huffman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-2

Query Match 100.0%; Score 30; DB 3; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCGTGTCCA 30
Db 1179 CATGCTTGTTCAACCGTTCGTCGTGTCCA 1208

RESULT 3
US-07-937-609-15
; Sequence 15, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: rat brain CCKB receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1494
US-07-937-609-15

Query Match 64.7%; Score 19.4; DB 2; Length 2243;
Best Local Similarity 79.3%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCGTGTCCA 29
Db 5 CCTGCTTGCTCAACTCTACGCTGTGTTC 33

RESULT 4
US-08-029-170-15
; Sequence 15, Application US/08029170
; Patent No. 6169173
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/029,170

FILING DATE: 19930310
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/937,609

FILING DATE: 02-SEP-1992
PRIOR APPLICATION NUMBER: US 07/928,033

FILING DATE: 11-AUG-1992
PRIOR APPLICATION NUMBER: US 07/861,769

FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/831,248

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD

TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109

TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs

TYPE: NUCLEIC ACID
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:
CLONE: rat brain CCKB receptor

FEATURE:
NAME/KEY: CDS

LOCATION: 136..1494
US-08-029-170-15

Query Match 64.7%; Score 19.4; DB 3; Length 2243;
Best Local Similarity 79.3%; Pred. No. 55;

Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 CATGCTGTGTTCAACCGTTGCTGTTGTTCC 29

Db 5 CCGCTGTGCTCAACTCTACGTTGTTTC 33

RESULT 5
US-09-443-745-15

Sequence 15, Application US/09443745
Patent No. 6706493

GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria

STATE: VA
COUNTRY: USA

ZIP: 22313-0299
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,745

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/029,170

FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609

FILING DATE: 02-SEP-1992
PRIOR APPLICATION NUMBER: US 07/928,033

FILING DATE: 11-AUG-1992
PRIOR APPLICATION NUMBER: US 07/861,769

FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/831,248

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD

TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109

TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs

TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA

IMMEDIATE SOURCE:
CLONE: rat brain CCKB receptor

FEATURE:
NAME/KEY: CDS

LOCATION: 136..1494
US-09-443-745-15

Query Match 64.7%; Score 19.4; DB 3; Length 2243;
Best Local Similarity 79.3%; Pred. No. 55;

Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 CATGCTGTGTTCAACCGTTGCTGTTGTTCC 29

Db 5 CCGCTGTGCTCAACTCTACGTTGTTTC 33

RESULT 6
US-09-949-016-16262

Sequence 16262, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16262

LENGTH: 45571
TYPE: DNA

ORGANISM: Human
US-09-949-016-16262

Query Match 63.3%; Score 19; DB 3; Length 45571;

Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TGCTGTGTTCAACCGTTCGTTGTTCC 29
|||
Db 38119 TGTTGTTTCATTCGTTCTTCTTCTCC 38145

RESULT 7

US-09-368-590-1/c
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
US-09-368-590-1

Query Match 62.7%; Score 18.8; DB 3; Length 7812;
Best Local Similarity 76.7%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTGTGTTCAACCGTTCGTTGTTCCA 30
|||
Db 841 CATGCTTCTGCAACAGGTCGTCTGCTCCA 812

RESULT 8

US-09-949-016-1438/c
; Sequence 1438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1438
; LENGTH: 8756
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1438

Query Match 62.7%; Score 18.8; DB 3; Length 8756;

Best Local Similarity 76.7%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTGTGTTCAACCGTTCGTTGTTCCA 30
|||
Db 1912 CATGCTTCTGCAACAGGTCGTCTGCTCCA 1883

RESULT 9

US-08-961-527-132
; Sequence 132, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-132

Query Match 62.7%; Score 18.8; DB 3; Length 9541;
Best Local Similarity 76.7%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTGTGTTCAACCGTTCGTTGTTCCA 30
|||
Db 8049 CAGCTTGTCCAAACGTTCCATTTTCCA 8078

RESULT 10

US-09-949-016-13180/c
; Sequence 13180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 13180
;; LENGTH: 112874
;; TYPE: DNA
;; ORGANISM: Human
;; NAME/KEY: misc feature
;; LOCATION: (1)...(112874)
;; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13180

Query Match 62.7%; Score 18.8; DB 3; Length 112874;
Best Local Similarity 76.7%; Pred. No. 2e+02; 7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATCTTGTTCACCGTTCCTCTTGTTC 30
Db 41167 CATCTTGTTCACCGTTCCTCTTGTTC 41138

RESULT 11

US-09-270-767-29480/c
; Sequence 29480, Application US/09270767
; Patent No. 6703491

;; GENERAL INFORMATION:

;; APPLICANT: Homburger et al.

;; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
;; FILE REFERENCE: File Reference: 7326-094

;; CURRENT APPLICATION NUMBER: US/09/270,767

;; CURRENT FILING DATE: 1999-03-17

;; NUMBER OF SEQ ID NOS: 62517

;; SOFTWARE: Patent in Ver. 2.0

;; SEQ ID NO 29480

;; LENGTH: 549

;; TYPE: DNA

;; ORGANISM: *Drosophila melanogaster*

US-09-270-767-29480

Query Match 62.0%; Score 18.6; DB 3; Length 549;
Best Local Similarity 84.0%; Pred. No. 98;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCCTCTTGT 27
Db 223 TGCTTGTTCACCGTTCCTCTTGT 199

RESULT 12

US-09-270-767-13492/c

;; Sequence 13492, Application US/09270767

;; Patent No. 6703491

;; GENERAL INFORMATION:

;; APPLICANT: Homburger et al.

;; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

;; FILE REFERENCE: File Reference: 7326-094

;; CURRENT APPLICATION NUMBER: US/09/270,767

;; CURRENT FILING DATE: 1999-03-17

;; NUMBER OF SEQ ID NOS: 62517

;; SOFTWARE: Patent in Ver. 2.0

;; SEQ ID NO 13492

;; LENGTH: 1120

;; TYPE: DNA

;; ORGANISM: *Drosophila melanogaster*

US-09-270-767-13492

Query Match 62.0%; Score 18.6; DB 3; Length 1120;
Best Local Similarity 84.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCCTCTTGT 27
Db 223 TGCTTGTTCACCGTTCCTCTTGT 199

RESULT 13

US-09-248-796A-3293

;; Sequence 3293, Application US/09248796A

;; Patent No. 6747137

;; GENERAL INFORMATION:

;; APPLICANT: Keith Weinstein et al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN.

;; FILE REFERENCE: 107196.132

;; CURRENT APPLICATION NUMBER: US/09/248,796A

;; CURRENT FILING DATE: 1999-02-12

;; PRIOR APPLICATION NUMBER: US 60/074,725

;; PRIOR FILING DATE: 1998-02-13

;; PRIOR APPLICATION NUMBER: US 60/096,409

;; PRIOR FILING DATE: 1998-08-13

;; NUMBER OF SEQ ID NOS: 28208

;; SEQ ID NO 3293

;; LENGTH: 1260

;; TYPE: DNA

;; ORGANISM: *Candida albicans*

US-09-248-796A-3293

Query Match 61.3%; Score 18.4; DB 3; Length 1260;
Best Local Similarity 78.8%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCCTCTTGTTC 30
Db 903 TGCTTGTTCACCGTTCCTCTTGTTC 930

RESULT 14

US-09-573-080A-7/c

;; Sequence 7, Application US/09573080A

;; Patent No. 6828097

;; GENERAL INFORMATION:

;; APPLICANT: JOAN, KNOLL

;; APPLICANT: ROGAN, PETER

;; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

;; FILE REFERENCE: 30307

;; CURRENT APPLICATION NUMBER: US/09/573,080A

;; CURRENT FILING DATE: 2000-05-16

;; NUMBER OF SEQ ID NOS: 479

;; SOFTWARE: Patent in version 3.0

;; SEQ ID NO 7

;; LENGTH: 2710

;; TYPE: DNA

;; ORGANISM: *Homo sapiens*

;; FEATURE:

;; NAME/KEY: repeat region

;; LOCATION: (1)..(2710)

;; OTHER INFORMATION: charlie3

;; NAME/KEY: misc feature

;; OTHER INFORMATION: n is a, c, g or t

;; PUBLICATION INFORMATION:

;; PUBLICATION INFORMATION:

;; AUTHORS: Jurka, J; Walichewicz, J; Milosavljevic, A

;; TITLE: Prototypic sequences for human repetitive DNA

;; JOURNAL: Journal of Molecular Evolution

;; VOLUME: 35

;; ISSUE: 4

;; PAGES: 286-291

;; DATE: 1992-10-

;; DATABASE ACCESSION NUMBER: Database for repetitive elements (repbase)

;; DATABASE ENTRY DATE: 1996-01-26

;; DATABASE ENTRY DATE: 1996-01-26

US-09-573-080A-7

Query Match 60.7%; Score 18.2; DB 3; Length 2710;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCTTGTTCACCGTTCGTCCTGTT 27
Db 1209 TGCTGTTTCACCACTTCGTCCTGTT 1185

RESULT 15
US-09-949-016-200252/c
; Sequence 200252, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200252
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-200252

Query Match 60.0%; Score 18; DB 3; Length 601;
Best Local Similarity 80.8%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 CTTGTTCAACCGTTCGTCCTGTTCCA 30
Db 239 CTTGTTAAACAGTTCCTGTTGCTCCA 214

Search completed: March 5, 2006, 22:36:22
Job time : 9.38752 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 23:29:31 ; Search time 43.1372 Seconds
(without alignments)
7550.985 Million cell updates/sec

Title: US-10-713-381-1_COPY_1179_1208
Perfect score: 30
Sequence: 1 catgctgttcacacgttcgtctgttcca 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	US-10-713-381-4	Sequence 4, Appli
2	30	100.0	255	US-10-713-381-9	Sequence 9, Appli
3	30	100.0	1394	US-10-713-381-1	Sequence 1, Appli
4	30	100.0	1394	US-10-713-381-2	Sequence 2, Appli
5	24.2	80.7	158	US-10-713-381-3	Sequence 3, Appli
C 6	22	73.3	1304	US-10-001-857-90	Sequence 90, Appli
C 7	21	70.0	1980090	US-10-719-993-6815	Sequence 6815, Ap
C 8	21	70.0	1980090	US-10-741-600-17676	Sequence 17676, A
9	20.4	68.0	1542	US-09-938-842A-1624	Sequence 1624, Ap
10	20.4	68.0	1542	US-09-938-842A-1624	Sequence 1624, Ap
11	20.2	67.3	2397	US-10-282-122A-31883	Sequence 31883, A
12	20	66.7	2000	US-10-260-238-1785	Sequence 1785, Ap
C 13	19.6	65.3	640	US-10-437-963-96639	Sequence 96639, A
C 14	19.6	65.3	901	US-10-425-115-3534	Sequence 3534, Ap
C 15	19.6	65.3	2000	US-10-260-238-1877	Sequence 1877, Ap
16	19.4	64.7	2243	US-09-443-745-15	Sequence 15, Appli
17	19.4	64.7	14655	US-11-083-391-15	Sequence 15, Appli
18	19.4	64.7	2256646	US-10-470-565-1	Sequence 1, Appli
19	19	63.3	822	US-09-925-065A-863989	Sequence 863989, A
20	19	63.3	964	US-09-925-065A-546217	Sequence 546217, A
C 21	19	63.3	1041	US-10-425-115-100318	Sequence 100318, A
C 22	19	63.3	1821	US-10-425-563-5	Sequence 5, Appli
C 23	19	63.3	1821	US-10-972-789A-5	Sequence 5, Appli

Sequence 729, App
Sequence 244, App
Sequence 472473,
Sequence 936359,
Sequence 936360,
Sequence 953397,
Sequence 279, App
Sequence 183, App
Sequence 971, App
Sequence 381, App
Sequence 183, App
Sequence 183, App
Sequence 771, App
Sequence 7281, App
Sequence 22639, A
Sequence 2194, Ap
Sequence 2195, Ap
Sequence 40048, A
Sequence 2217, Ap
Sequence 9220, Ap
Sequence 37788, A
Sequence 2535, Ap
Sequence 33483, A

24 19 63.3 5671 3 US-09-764-872-729
25 19 63.3 198522 5 US-10-087-192-244
26 18.8 62.7 520 4 US-09-925-065A-472473
27 18.8 62.7 593 4 US-09-925-065A-936359
28 18.8 62.7 593 4 US-09-925-065A-936360
29 18.8 62.7 593 4 US-09-925-065A-953397
30 18.8 62.7 883 3 US-09-934-455-279
C 31 18.8 62.7 883 6 US-10-225-068-183
C 32 18.8 62.7 883 6 US-10-225-068A-971
C 33 18.8 62.7 883 7 US-10-374-780A-381
C 34 18.8 62.7 883 9 US-10-225-068-183
C 35 18.8 62.7 883 9 US-10-225-068A-971
C 36 18.8 62.7 1083 3 US-09-815-242-7281
C 37 18.8 62.7 1083 7 US-10-282-122A-22639
C 38 18.8 62.7 1083 7 US-10-335-977-2194
C 39 18.8 62.7 1225 7 US-10-437-963-40048
C 40 18.8 62.7 1856 7 US-10-472-928-2217
C 41 18.8 62.7 1859 8 US-09-815-242-9220
C 42 18.8 62.7 1902 3 US-10-282-122A-37788
C 43 18.8 62.7 1902 7 US-10-260-238-2535
C 44 18.8 62.7 2000 7 US-10-369-493-33483
C 45 18.8 62.7 2247 6

ALIGNMENTS

RESULT 1

US-10-713-381-4
; Sequence 4, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GRENFAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-4

Query Match 100.0%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.008; 0; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTGTTCACCGTTCGTTCTTCTTCCA 30

Db 1 CATGCTGTTCACCGTTCGTTCTTCTTCCA 30

RESULT 2

US-10-713-381-9
; Sequence 9, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GRENFAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME

; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9

Query Match 100.0%; Score 30; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 30
|||||
Db 39 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 68

RESULT 3

US-10-713-381-1
; Sequence 1, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-1

Query Match 100.0%; Score 30; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 30
|||||
Db 1179 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 1208

RESULT 4

US-10-713-381-2
; Sequence 2, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-2

Query Match 100.0%; Score 30; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 30
|||||
Db 1179 CATGCTTGTTCAACCGTTCGTCCTGTGTTCCA 1208

RESULT 5

US-10-713-381-3
; Sequence 3, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3

Query Match 80.7%; Score 24.2; DB 8; Length 158;
Best Local Similarity 89.7%; Pred. No. 2.8;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCAACCGTTCGTCCTGTGTTCC 29
|||||
Db 25 CATGCTTGTTCAACCGTTCGTCCTGTGTTCC 53

RESULT 6

US-10-001-857-90/c
; Sequence 90, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-001-857-90

Query Match 73.3%; Score 22; DB 5; Length 1304;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CATGCTGTTCAACCGTTCGTCCTGTGTTCCA 30
DB 1155 CTTTCTGTTCCCGTTCCTCTGTGTTCCA 1126

RESULT 7

US-10-719-993-6815/c
; Sequence 6815, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01496
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6815
; LENGTH: 1980090
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6815

Query Match 70.0%; Score 21; DB 8; Length 1980090;
Best Local Similarity 82.8%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCAACCGTTCGTCCTGTGTTCCA 30
DB 1948918 ATTCTGCTGAACAGTTCGTCCTGTGTTACCA 1948890

RESULT 8

US-10-741-600-17676/c
; Sequence 17676, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17676
; LENGTH: 1980090
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17676

Query Match 70.0%; Score 21; DB 8; Length 1980090;
Best Local Similarity 82.8%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCTGTTCAACCGTTCGTCCTGTGTTCCA 30
DB 1948918 ATTCTGCTGAACAGTTCGTCCTGTGTTACCA 1948890

RESULT 9

US-09-938-842A-1624
; Sequence 1624, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1624
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1624

Query Match 68.0%; Score 20.4; DB 3; Length 1542;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATGCTGTTCAACCGTTCGTCCTGTGTTCCA 30
DB 237 CATGATTGTTCAACCAATCGTCGGTTTCCA 266

RESULT 10

US-09-938-842A-1624
; Sequence 1624, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; CURRENT APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1624
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1624

Query Match 68.0%; Score 20.4; DB 3; Length 1542;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATGCTGTTCAACCGTTCGTCCTGTGTTCCA 30
DB 237 CATGATTGTTCAACCAATCGTCGGTTTCCA 266

US-10-282-122A-31883
; Sequence 31883, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvakind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31883
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31883
Query Match 67.3%; Score 20.2; DB 7; Length 2397;
Best Local Similarity 88.0%; Pred. No. 2e+02; 3; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;
QY 1 CATGCTGTTCACCGTTCGTCCTTG 25
Db 516 CATGCTGTTCACCGTTCGTCCTTG 540
RESULT 12
US-10-260-238-1785
; Sequence 1785, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel

APPLICANT: Provart, Nicholas
APPLICANT: Riche, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1785
LENGTH: 2000
TYPE: DNA
ORGANISM: Oryza sativa
US-10-260-238-1785
Query Match 66.7%; Score 20; DB 7; Length 2000;
Best Local Similarity 82.1%; Pred. No. 2.3e+02; 5; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 5;
QY 3 TGTCTGTTCAACCGTTCGTCCTTGTTCCA 30
Db 1179 TACATGTTTAAACCGTTCGTCCTTATTCAA 1206
RESULT 13
US-10-437-963-96639/c
; Sequence 96639, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 96639
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94716C.1
US-10-437-963-96639
Query Match 65.3%; Score 19.6; DB 7; Length 640;
Best Local Similarity 84.6%; Pred. No. 2.9e+02; 4; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;
QY 5 CTGTGTTCAACCGTTCGTCCTTGTTCCA 30
Db 199 CATGTTTAAACCGTTCGTCCTTATTCAA 174
RESULT 14
US-10-425-115-3534/c
; Sequence 3534, Application US/10425115
; Publication No. US200400214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 3534
 ; LENGTH: 901

; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_103225C.1
 US-10-425-115-3534

Query Match 65.3%; Score 19.6; DB 8; Length 901;
 Best Local Similarity 84.6%; Pred. No. 3.1e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATGCTTTCAACCGTTCGTCTGT 26
 DB 33 CAGCTTTGTTCAACCGTTCGTGT 8

RESULT 15

US-10-260-238-1977/c
 ; Sequence 1977, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 1977
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-10-260-238-1977

Query Match 65.3%; Score 19.6; DB 7; Length 2000;
 Best Local Similarity 84.6%; Pred. No. 3.4e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CTTGTTCAACCGTTCGTCTGTCCA 30
 DB 291 CATGTTTAAACCGTTCGTCTATTCAA 266

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 Job time : 47.1372 secs

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Wed Mar 8 14:16:28 2006

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Page 1

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OM nucleic - nucleic search, using sw model

Run on: March 6, 2006, 01:58:03 ; Search time 31.3166 Seconds
(without alignments)
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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	64.7	2422	US-11-136-527-2272	Sequence 2272, Ap
2	19	63.3	622	US-09-925-065A-863989	Sequence 863989
3	19	63.3	964	US-09-925-065A-546217	Sequence 546217
C 4	18.8	62.7	1821	US-11-197-133A-5	Sequence 5, Appl1
5	18.8	62.7	520	US-09-925-065A-472473	Sequence 472473
6	18.8	62.7	593	US-09-925-065A-936359	Sequence 936359
7	18.8	62.7	593	US-09-925-065A-936360	Sequence 936360
8	18.8	62.7	593	US-09-925-065A-953397	Sequence 953397
C 9	18.8	62.7	1908	US-10-523-503-37	Sequence 37, Appl1
10	18.8	62.7	128963	US-10-330-773-86	Sequence 86, Appl1
11	18.4	61.3	599	US-09-925-065A-811550	Sequence 811550, A
12	18.4	61.3	624	US-09-925-065A-772237	Sequence 772237
C 13	18.4	61.3	629	US-09-925-065A-787145	Sequence 787145
14	18.4	61.3	642	US-09-925-065A-423	Sequence 423, App
15	18.4	61.3	1012	US-10-750-185-52713	Sequence 52713, A
16	18.4	61.3	1012	US-10-750-623-52713	Sequence 52713, A
C 17	18.4	61.3	1257	US-10-750-185-64410	Sequence 64410, A
18	18.4	61.3	1257	US-10-750-623-64410	Sequence 64410, A
C 19	18.4	61.3	1354	US-09-925-065A-70688	Sequence 70688, A
20	18.4	61.3	1354	US-09-925-065A-70689	Sequence 70689, A

C 21	18	60.0	572	6	US-09-925-065A-819344	Sequence 819344,
22	18	60.0	573	6	US-09-925-065A-821053	Sequence 821053,
23	18	60.0	1395	6	US-09-925-065A-30378	Sequence 30378, A
24	18	60.0	1395	6	US-09-925-065A-30379	Sequence 30379, A
25	17.8	59.3	201	8	US-10-995-561-9774	Sequence 9774, Ap
26	17.8	59.3	201	8	US-10-995-561-9787	Sequence 9787, Ap
27	17.8	59.3	201	8	US-10-995-561-52210	Sequence 52210, A
28	17.8	59.3	603	6	US-09-925-065A-826915	Sequence 826915, A
29	17.8	59.3	617	6	US-09-925-065A-673672	Sequence 673672,
30	17.8	59.3	617	6	US-09-925-065A-673673	Sequence 673673,
31	17.8	59.3	652	6	US-09-925-065A-667982	Sequence 667982,
32	17.8	59.3	1385	6	US-09-925-065A-716810	Sequence 716810,
33	17.8	59.3	1385	6	US-11-010-239-68	Sequence 68, Appl
34	17.8	59.3	2039	6	US-09-925-065A-704153	Sequence 704153,
35	17.8	59.3	2039	6	US-09-925-065A-704154	Sequence 704154,
36	17.8	59.3	2039	6	US-09-925-065A-704155	Sequence 704155,
37	17.8	59.3	2867	8	US-10-995-561-357	Sequence 357, App
38	17.8	59.3	3431	8	US-10-995-561-358	Sequence 358, App
39	17.8	59.3	9474	12	US-11-155-232-1	Sequence 1, Appl1
40	17.8	59.3	45038	8	US-10-995-561-13311	Sequence 13311, A
41	17.8	59.3	81210	8	US-10-995-561-13295	Sequence 13295, A
C 42	17.8	59.3	163317	12	US-11-117-187-212	Sequence 212, App
43	17.8	59.3	171732	12	US-11-121-086-98	Sequence 98, Appl
44	17.8	59.3	1082144	12	US-11-117-187-211	Sequence 211, App
45	17.6	58.7	600	12	US-11-136-527-7828	Sequence 7828, Ap

ALIGNMENTS

RESULT 1
US-11-136-527-2272
; Sequence 2272, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI1086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO. 2272
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2272

Query Match Best Local Similarity 64.7%; Score 19.4; DB 12; Length 2422;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CATCTTGTTCACCGTTCGTCCTGTTC 29
DB 5 CCTGCTTGCTCAACTCTACGCTCTGTTTC 33

RESULT 2
US-09-925-065A-863989
; Sequence 863989, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 863989
;; LENGTH: 622
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-863989

Query Match 63.3%; Score 19; DB 6; Length 622;
Best Local Similarity 81.5%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCTTGTTCACCGTTCGTTCTTGTTC 28
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Db 400 AGGCTAGTCCAACTTTGTCTGTTC 426

RESULT 3
US-09-925-065A-546217
;; Sequence 546217, Application US/09925065A
;; Publication No. US20040181048A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;; CURRENT APPLICATION NUMBER: US/09/925.065A
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 546217
;; LENGTH: 964
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-546217

Query Match 63.3%; Score 19; DB 6; Length 964;
Best Local Similarity 81.5%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCTTGTTCACCGTTCGTTCTTGTTC 28
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Db 256 AGGCTAGTCCAACTTTGTCTGTTC 282

RESULT 4
US-11-197-133A-5/c
;; Sequence 5, Application US/11197133A
;; Publication No. US20060040361A1
;; GENERAL INFORMATION:
;; APPLICANT: De Le Fuente Jose de Jesus
;; APPLICANT: Kocan Katherine M.
;; APPLICANT: Garcia-Almazan Consuelo
;; APPLICANT: Blouin Edwin F.
;; TITLE OF INVENTION: Protective antigens and vaccines for the control of multi species

;; TITLE OF INVENTION: Infestations
;; FILE REFERENCE: 57338/05-261
;; CURRENT APPLICATION NUMBER: US/11/197,133A
;; CURRENT FILING DATE: 2005-08-04
;; PRIOR APPLICATION NUMBER: US 10/972789
;; PRIOR FILING DATE: 2004-10-25
;; PRIOR APPLICATION NUMBER: US 10/425563
;; PRIOR FILING DATE: 2003-04-29
;; PRIOR APPLICATION NUMBER: US 60/376251
;; PRIOR FILING DATE: 2002-04-29
;; NUMBER OF SEQ ID NOS: 62
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 5
;; LENGTH: 1821
;; TYPE: DNA
;; ORGANISM: Ixodes scapularis
;; FEATURE:
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US-11-197-133A-5
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Best Local Similarity 81.5%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 TGGTTGTTCACCGTTCGTTCTTGTTC 29
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Db 914 TGGTTGTTCACCGTTCGTTCTTGTTC 888
RESULT 5
US-09-925-065A-472473/c
;; Sequence 472473, Application US/09925065A
;; Publication No. US20040181048A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;; CURRENT APPLICATION NUMBER: US/09/925.065A
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086


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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-523-503-37

Query Match      62.7%; Score 18.8; DB 7; Length 1908;
Best Local Similarity 76.7%; Pred. No. 51;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGTCCTGTTCCTCA 30
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Db 1688 CTTGCTTCTTCGACCGTTCCTTTTGGTTCCA 1659

RESULT 10
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; Sequence 86, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 128963
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
; LOCATION: (1)...(128963)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-86

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Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 102327 CAAGTTCTTCACCGTTCCTCATGTGCACA 102298

RESULT 11
US-09-925-065A-811550
; Sequence 811550, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 811550
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-811550
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Query Match      61.3%; Score 18.4; DB 6; Length 599;
Best Local Similarity 78.6%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCCTTGTTCACCGTTCGTCCTGTTCCTCA 30
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Db 504 TGCCTTGTTCACCGTTCGTCCTGTTCCTCA 531

RESULT 12
US-09-925-065A-772237
; Sequence 772237, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772237
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-772237

Query Match      61.3%; Score 18.4; DB 6; Length 624;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCTTGTTCACCGTTCGTCCTGTTCCTCC 29
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Db 49 ATTTTGTTCACCTGTCGTCCTGTTCCTC 76

RESULT 13
US-09-925-065A-787145/c
; Sequence 787145, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 787145
; LENGTH: 629
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-787145

Query Match 61.3%; Score 18.4; DB 6; Length 629;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 ATGCTTGTCAACCGTTCGTCCTGTTCC 29
DB 576 ATTTTGTTCACACTGTCGTCGTTTC 549

RESULT 14
US-09-925-065A-423
Sequence 423, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 423
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-423

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Best Local Similarity 78.6%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 295 TGCTTGTCTCTCCATTCGTCCTTTGCCA 322

RESULT 15
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Sequence 52713, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 52713
LENGTH: 1012

TYPE: DNA
ORGANISM: Bovine
US-10-750-185-52713

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Best Local Similarity 78.6%; Pred. No. 67;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 454 ATTTTGTTCACCGTTCGTCCTGTTCC 481

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Job time : 33.3166 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	100.0	30	25	US-09-504-487-4	Sequence 4, Appli
2	30	100.0	30	57	US-10-713-381-4	Sequence 9, Appli
3	30	100.0	255	57	US-09-504-487-9	Sequence 9, Appli
4	30	100.0	255	57	US-10-713-381-9	Sequence 1, Appli
5	30	100.0	1394	25	US-09-504-487-1	Sequence 2, Appli
6	30	100.0	1394	25	US-09-504-487-2	Sequence 1, Appli
7	30	100.0	1394	57	US-10-713-381-1	Sequence 2, Appli
8	30	100.0	1394	57	US-10-713-381-2	Sequence 3, Appli
9	24.2	80.7	158	25	US-09-504-487-3	Sequence 3, Appli
10	24.2	80.7	158	25	US-10-713-381-3	Sequence 3, Appli
11	22	73.3	1304	40	US-10-001-857-90	Sequence 90, Appli
12	21.2	70.7	724	43	US-10-060-063-4003	Sequence 4003, Ap
13	21.2	70.7	724	43	US-10-266-090-4003	Sequence 4003, Ap
14	21.2	70.7	2221	31	US-09-702-134-51486	Sequence 51486, A
15	21.2	70.7	2221	31	US-09-815-264-109207	Sequence 109207,
16	21.2	70.7	2264	28	US-09-620-392-39678	Sequence 39678, A
17	21.2	70.7	14154	28	US-09-620-392-62193	Sequence 62193, A
18	21.2	70.7	14154	31	US-09-702-134-1310	Sequence 1310, Ap
19	21.2	70.7	14154	33	US-09-815-264-61559	Sequence 61559, A
20	21.2	70.7	18423	28	US-09-620-392-18275	Sequence 18275, A
21	21.2	70.7	18423	31	US-09-702-134-27508	Sequence 27508, A
22	21.2	70.7	18423	33	US-09-815-264-81379	Sequence 81379, A
23	21.2	70.7	18716	28	US-09-620-392-5157	Sequence 5157, Ap

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28 21 70-0 7201 33 US-09-815-264-77757 Sequence 77757, A
29 21 70-0 7327 38 US-09-620-392-20710 Sequence 20710, A
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31 21 70-0 10046 38 US-09-620-392-36220 Sequence 36220, A
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41 21 70-0 19966 31 US-09-702-134-25989 Sequence 25989, A
42 21 70-0 19966 33 US-09-815-264-79560 Sequence 79560, A
43 21 70-0 27229 28 US-09-620-392-594 Sequence 594, App
44 21 70-0 27229 31 US-09-702-134-25714 Sequence 25714, A
45 21 70-0 27229 33 US-09-815-264-73378 Sequence 73378, A

ALIGNMENTS

RESULT 1
US-09-504-487-4
; Sequence 4, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-09-504-487-4
Query Match 100.0%; Score 30; DB 25; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATGCTTGTCAACCGTTCGTCCTGTGTTCCA 30
Db 1 CATGCTTGTCAACCGTTCGTCCTGTGTTCCA 30
RESULT 2
US-10-713-381-4
; Sequence 4, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381

; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-4
Query Match 100.0%; Score 30; DB 57; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATGCTTGTCAACCGTTCGTCCTGTGTTCCA 30
Db 1 CATGCTTGTCAACCGTTCGTCCTGTGTTCCA 30
RESULT 3
US-09-504-487-9
; Sequence 9, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-09-504-487-9
Query Match 100.0%; Score 30; DB 25; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CATGCTTGTCAACCGTTCGTCCTGTGTTCCA 30
Db 39 CATGCTTGTCAACCGTTCGTCCTGTGTTCCA 68
RESULT 4
US-10-713-381-9
; Sequence 9, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255

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; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9

Query Match      100.0%; Score 30; DB 57; Length 255;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATGCTGTTCACCGTTCGTCCTGTGTCCA 30
DB      39 CATGCTGTTCACCGTTCGTCCTGTGTCCA 68

RESULT 5
US-09-504-487-1
; Sequence 1, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-09-504-487-1

Query Match      100.0%; Score 30; DB 25; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATGCTGTTCACCGTTCGTCCTGTGTCCA 30
DB      1179 CATGCTGTTCACCGTTCGTCCTGTGTCCA 1208

RESULT 6
US-09-504-487-2
; Sequence 2, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-09-504-487-2

Query Match      100.0%; Score 30; DB 25; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CATGCTGTTCACCGTTCGTCCTGTGTCCA 30
DB      1179 CATGCTGTTCACCGTTCGTCCTGTGTCCA 1208

RESULT 7
US-10-713-381-1
; Sequence 1, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-1

Query Match      100.0%; Score 30; DB 57; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATGCTGTTCACCGTTCGTCCTGTGTCCA 30
DB      1179 CATGCTGTTCACCGTTCGTCCTGTGTCCA 1208

RESULT 8
US-10-713-381-2
; Sequence 2, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE-TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-2

Query Match      100.0%; Score 30; DB 57; Length 1394;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATGCTGTTCACCGTTCGTCCTGTGTCCA 30
DB      1179 CATGCTGTTCACCGTTCGTCCTGTGTCCA 1208

RESULT 9
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US-09-504-487-3
; Sequence 3, Application US/09504487
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/09/504,487
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-09-504-487-3

Query Match      80.7%; Score 24.2; DB 25; Length 158;
Best Local Similarity 89.7%; Pred. No. 7.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGCTTGTTC 29
Db 25 CATGCTTGTTCACCGTTCGCTTGTTC 53

RESULT 10
US-10-713-381-3
; Sequence 3, Application US/10713381
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3

Query Match      80.7%; Score 24.2; DB 57; Length 158;
Best Local Similarity 89.7%; Pred. No. 7.5;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGCTTGTTC 29
Db 25 CATGCTTGTTCACCGTTCGCTTGTTC 53

RESULT 11
US-10-001-857-90/c
; Sequence 90, Application US/10001857
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heirve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
```

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US-10-001-857-90
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-857-90

Query Match      73.3%; Score 22; DB 40; Length 1304;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CATGCTTGTTCACCGTTCGCTTGTTC 30
Db 1155 CTTCTGTTCCTCCCGTTCCTTGTTC 1126

RESULT 12
US-10-060-063-4003
; Sequence 4003, Application US/10060063
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-Lin
; APPLICANT: Goff, Stephen A.
; TITLE OF INVENTION: CEREAL SIMPLE SEQUENCE REPEAT MARKERS
; FILE REFERENCE: NADII 026A
; CURRENT APPLICATION NUMBER: US/10/060,063
; CURRENT FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 9099
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4003
; LENGTH: 724
; TYPE: DNA
; ORGANISM: RICE
US-10-060-063-4003

Query Match      70.7%; Score 21.2; DB 40; Length 724;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTGTTCACCGTTCGCTTGTTC 30
Db 529 CATGTTTACCGTTCGCTTGTTC 554

RESULT 13
US-10-266-090-4003
; Sequence 4003, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GORF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII 058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4003
; LENGTH: 724
; TYPE: DNA
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ORGANISM: ORYZA SATIVA
US-10-266-090-4003

Query Match 70.7%; Score 21.2; DB 43; Length 724;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGTTCACCGTTCGTCCTTTTCCA 30
DB 833 CATGTTTAAACGTCGTCCTTTTCCA 858

Search completed: March 6, 2006; 09:38:09
Job time : 270.366 secs

RESULT 14
US-09-702-134-51486
; Sequence 51486, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 51486
; LENGTH: 2221
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-51486

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Best Local Similarity 88.5%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTGTTCACCGTTCGTCCTTTTCCA 30
DB 833 CATGTTTAAACGTCGTCCTTTTCCA 858

RESULT 15
US-09-815-264-109207
; Sequence 109207, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 109207
; LENGTH: 2221
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-109207

Query Match 70.7%; Score 21.2; DB 33; Length 2221;
Best Local Similarity 88.5%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb.ov.*

6: gb.pat.*

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9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.hcg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	40	6 AX224399	AX224399 Sequence
2	40	100.0	50	6 AX224398	AX224398 Sequence
3	40	100.0	158	6 AX224396	AX224396 Sequence
4	40	100.0	255	6 AX224402	AX224402 Sequence
5	40	100.0	1394	6 BD062176	BD062176 Male tiss
6	40	100.0	1394	6 BD062177	BD062177 Male tiss
7	40	100.0	1394	6 AX224394	AX224394 Sequence
8	40	100.0	1394	6 AX224395	AX224395 Sequence
9	40	100.0	3343	15 AF360356	AF360356 Zea mays
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11	30.4	76.0	137327	15 AC135206	AC135206 Oryza sat
12	25.2	63.0	103308	14 AC158670	AC158670 Bos tauri
13	24	60.0	55001	8 AC084230	AC084230 Homo sapi
14	24	60.0	127196	9 AL080784	AL080784 Mouse DNA
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16	24	60.0	171940	14 AC148514	AC148514 Papio anu
17	24	60.0	216548	14 AC161620	AC161620 Pan trogl
18	23.6	59.0	193735	14 AC148501	AC148501 Callithri

C 19	23.2	58.0	170392	14	AC156784	AC156784 Rhinolph
C 20	23.2	58.0	182816	14	AC160916	AC160916 Rhinolph
C 21	23.2	58.0	211584	9	AC153927	AC153927 Mus muscu
C 22	23	57.5	52648	5	CR788256	CR788256 Zebrafish
C 23	23	57.5	117026	8	AC008897	AC008897 Homo sapi
C 24	23	57.5	153971	9	AC102478	AC102478 Mus muscu
C 25	23	57.5	177104	14	AC125876	AC125876 Rattus no
C 26	23	57.5	195285	4	CR847932	CR847932 Danio rer
C 27	23	57.5	218224	9	AC134404	AC134404 Mus muscu
C 28	23	57.5	234163	14	AC115318	AC115318 Rattus no
C 29	23	57.5	235286	14	AC159385	AC159385 Bos tauru
C 30	23	57.5	242109	14	AC147523	AC147523 Otollemur
C 31	23	57.5	319056	14	AC101660	AC101660 Homo sapi
C 32	22.8	57.0	164944	2	AC008195	AC008195 Drosophil
C 33	22.8	57.0	175781	2	AC008091	AC008091 Drosophil
C 34	22.8	57.0	235928	2	AB003726	AB003726 Drosophil
C 35	22.8	57.0	309657	14	AC157205	AC157205 Bos tauru
C 36	22.6	56.5	90463	14	AC165458	AC165458 Bos tauru
C 37	22.6	56.5	95896	8	AL356384	AL356384 Human DNA
C 38	22.6	56.5	129410	14	AC149638	AC149638 Medicago
C 39	22.6	56.5	160246	14	AC009221	AC009221 Homo sapi
C 40	22.6	56.5	161817	9	AC132119	AC132119 Mus muscu
C 41	22.6	56.5	170973	8	AP000923	AP000923 Homo sapi
C 42	22.6	56.5	175110	8	AP002428	AP002428 Homo sapi
C 43	22.6	56.5	186457	14	AC129669	AC129669 Rattus no
C 44	22.6	56.5	196990	14	AC134013	AC134013 Rattus no
C 45	22.6	56.5	235953	14	AC130117	AC130117 Rattus no

ALIGNMENTS

RESULT 1	AX224399	Sequence 6 from Patent WO0160997.	40 bp	DNA	linear	PAT 10-SEP-2001
LOCUS	AX224399					
DEFINITION	Sequence 6 from Patent WO0160997.					
ACCESSION	AX224399					
VERSION	AX224399.1	GI:15554641				
KEYWORDS	Zea mays					
SOURCE	Zea mays					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	1	Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.				
AUTHORS	Male tissue-preferred regulatory region and method of using same					
TITLE	Patent: WO 0160997-A 6 23-AUG-2001;					
JOURNAL	PIONEER HI-BRED INTERNATIONAL, INC. (US)					
FEATURES	Location/Qualifiers					
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	/organism="Zea mays"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:4577"					
ORIGIN						
Query Match	100.0%; Score 40; DB 6; Length 40;					
Best Local Similarity	100.0%; Pred. No. 0.00011;					
Matches	40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 AGGATCCTCTCTCCCAACATCCATCTTACTCTATGTCGCAAC 40					
Db	1 AGGATCCTCTCTCCCAACATCCATCTTACTCTATGTCGCAAC 40					
RESULT 2	AX224398	Sequence 5 from Patent WO0160997.	50 bp	DNA	linear	PAT 10-SEP-2001
LOCUS	AX224398					
DEFINITION	Sequence 5 from Patent WO0160997.					
ACCESSION	AX224398					
VERSION	AX224398.1	GI:15554640				
KEYWORDS	Zea mays					
SOURCE	Zea mays					

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ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 5 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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DEFINITION Sequence 3 from Patent WO0160997.
ACCESSION AX224396
VERSION AX224396.1 GI:15554638
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SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 3 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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ACCESSION AX224402
VERSION AX224402.1 GI:15554644
KEYWORDS Zea mays
SOURCE Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same

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JOURNAL Patent: WO 0160997-A 9 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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LOCUS BD062176 1394 bp DNA linear PAT 27-AUG-2002
DEFINITION Male tissue-preferred regulatory region and method of using same.
ACCESSION BD062176
VERSION BD062176.1 GI:22607781
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Hominiidae; Homo.
1 (bases 1 to 1394)
REFERENCE Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A. and
AUTHORS Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: JP 2001520523-A 1 30-OCT-2001;
PIONEER HI BRED INTERNATIONAL INC
COMMENT PN JP 2001520523-A/1
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAAT,GARY A HUFFMAN,
TIMMY L KENDALL
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LOCUS BD062177 1394 bp DNA linear PAT 27-AUG-2002
DEFINITION Male tissue-preferred regulatory region and method of using same.
ACCESSION BD062177
VERSION BD062177.1 GI:22607782
KEYWORDS JP 2001520523-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo;
1 (bases 1 to 1394)
Albertsen M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
Patent: JP 2001520523-A 23-OCT-2001;
PIONEER HI-BRED INTERNATIONAL INC
JP 2001520523-A/2
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAAT, GARY A HUFFMAN,
TIMMY L KENDALL
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ACCESSION AX224394
VERSION AX224394.1 GI:15554636
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clade; Panicoideae; Andropogoneae; Zea.
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Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
Patent: WO 0160997-A 1 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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AX224395 1394 bp DNA linear PAT 10-SEP-2001
LOCUS
DEFINITION Sequence 2 from Patent WO0160997.
ACCESSION AX224395
VERSION AX224395.1 GI:15554637
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clade; Panicoideae; Andropogoneae; Zea.
1
Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
Patent: WO 0160997-A 2 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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LOCUS
DEFINITION Zea mays male fertility protein (Me45) gene, complete cds.
ACCESSION AF360356
VERSION AF360356.1 GI:14028756
KEYWORDS
SOURCE Zea mays
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clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3343)
Fox, T.W., Trimmell, M.R. and Albertsen, M.C.
Cloning of Me45, a gene required for male fertility from Zea mays
Unpublished
2 (bases 1 to 3343)
Fox, T.W., Trimmell, M.R. and Albertsen, M.C.
Direct Submission
Submitted (13-MAR-2001) Trait and Technology Development; Pioneer
HI-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,
IA 50131-1004, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo;
1 (bases 1 to 1394)
Albertsen M.C., Fox, T.W., Garnaat, C.W., Huffman, G.A. and
Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
Patent: JP 2001520523-A 23-OCT-2001;
PIONEER HI-BRED INTERNATIONAL INC
JP 2001520523-A/2
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ACCESSION AX224394
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KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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clade; Panicoideae; Andropogoneae; Zea.
1
Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
Patent: WO 0160997-A 1 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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RESULT 8
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ACCESSION AX224395
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Albertsen, M.C., Fox, T.W., Garnaat, C.W., Huffman, G. and Kendall, T.L.
Male tissue-preferred regulatory region and method of using same
Patent: WO 0160997-A 2 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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RESULT 9
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LOCUS
DEFINITION Zea mays male fertility protein (Me45) gene, complete cds.
ACCESSION AF360356
VERSION AF360356.1 GI:14028756
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clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3343)
Fox, T.W., Trimmell, M.R. and Albertsen, M.C.
Cloning of Me45, a gene required for male fertility from Zea mays
Unpublished
2 (bases 1 to 3343)
Fox, T.W., Trimmell, M.R. and Albertsen, M.C.
Direct Submission
Submitted (13-MAR-2001) Trait and Technology Development; Pioneer
HI-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston,
IA 50131-1004, USA
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WPCOMMENT

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 AP008209_191 19100001 19210000
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 AP008209_193 19300001 19410000
 AP008209_194 19400001 19510000
 AP008209_195 19500001 19610000
 AP008209_196 19600001 19710000

Query Match. 76.0%; Score 30.4; DB 15; Length 110000;
 Best Local Similarity 85.0%; Pred. No. 0.18;
 Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCAATCTTACTCATGCAAC 40
 |||||
 Db 36341 AGAACACCTACTCCCAACATCAATGCTGCTCATGCAAC 36302

RESULT 11
 AC135206/c 137327 bp DNA linear PLN 16-APR-2003
 LOCUS Oryza sativa (japonica cultivar-group) chromosome 3 clone
 Q31041802, complete sequence.

ACCESSION AC135206
 VERSION AC135206.3 GI:27596977
 KEYWORDS HTG
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Currie, J. and Collura, K.
 TITLE Rice Genomic Sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Saski, C., Currie, J., Collura, K. and Thompson, S.
 TITLE Direct Submission
 JOURNAL Submitted (09-OCT-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
 REFERENCE 3 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Saski, C., Currie, J., Collura, K. and Thompson, S.
 TITLE Direct Submission
 JOURNAL Submitted (06-NOV-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
 REFERENCE 4 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Currie, J., Collura, K. and Thompson, S.
 TITLE Direct Submission
 JOURNAL Submitted (11-JAN-2003) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
 REFERENCE 5 (bases 1 to 137327)
 AUTHORS Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H., Rambo, T., Saski, C., Henry, D., Thompson, S., Simmons, J., Thurmond, S.K. and Sun, S.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2003) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
 COMMENT On Jan 11, 2003 this sequence version replaced gi:24635891.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32874 and at area 19945-13212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69857-70761, 89836-90416, 98951-99009, 105315-105507, and 133052-133152 are covered by Monsanto only. The nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.

FEATURES
 source
 1. 137327
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39947"
 /chromosome="3"
 /clone="OU1041F02"

RESULT 12
 AC156670
 LOCUS
 DEFINITION
 AC156670
 AC156670.2 GI:68266432
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
 Bos taurus (cow)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 303308)
 Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
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 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotco, M., Eugene, C., Evans, C.A., Falls, I., Fan, G.,
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 Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gebregorgis, E., Geer, K., Gill, R., Grady, N., Guerra, W., Guevara, W.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
 Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
 Hollins, B., Howell, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
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 Manjun, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwakoemeh, O., Okwuonu, G., Olampunsgoon, A., Pal, S., Parks, K.,
 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Plopper, F., Ponder, A., Popovic, D., Primus, E., Pu, L.-L.,
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 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
 Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
 Sanders, M., Saverly, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
 Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajic, D.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,
 Williams, G., Willson, R., Wlezyk, R., Woodson, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, D., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Welser, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 303308)
 Morley, K.C.
 Direct Submission
 Submitted (03-FEB-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

3 (bases 1 to 303308)
 Cow Genome Sequencing Consortium.
 Direct Submission
 Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jun 28, 2005 this sequence version replaced gi:58531390.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/) Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

COMMENT

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: FDUU
 Center clone name: CH240-60K24
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 284059 bases at least Q40
 Consensus quality: 288397 bases at least Q30
 Consensus quality: 292413 bases at least Q20
 Estimated insert size: 289468; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * NOTE: This sequence may represent more than one clone.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 48 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 4448: contig of 4448 bp in length
 4498: gap of 50 bp
 4499 14243: contig of 9745 bp in length
 14244 14293: gap of 50 bp
 14294 35369: contig of 21076 bp in length
 35419: gap of 50 bp
 35420 47505: contig of 12086 bp in length
 47506 47555: gap of 50 bp
 47556 49432: contig of 1877 bp in length
 49433 49482: gap of 50 bp
 49483 51615: contig of 2133 bp in length
 51616 52521: gap of 906 bp
 52522 59438: contig of 6917 bp in length
 59439 59488: gap of 50 bp
 64821: contig of 3333 bp in length
 64822 64871: gap of 50 bp
 64872 74540: contig of 9669 bp in length
 74541 74590: gap of 50 bp
 74591 90360: contig of 15770 bp in length
 90361 90833: gap of 473 bp
 90834 100046: contig of 9213 bp in length
 100047 100096: gap of 50 bp
 100097 104650: contig of 4554 bp in length
 104651 104950: gap of 300 bp
 104951 106450: contig of 1500 bp in length
 106451 106608: gap of 158 bp
 106609 109787: contig of 3179 bp in length


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* 109788 109837: gap of 50 bp
* 109838 121211: contig of 11374 bp in length
* 121212 121261: gap of 50 bp
* 121262 131158: contig of 9897 bp in length
* 131159 131208: gap of 50 bp
* 131209 139112: contig of 7904 bp in length
* 139113 139162: gap of 50 bp
* 139163 145938: contig of 6776 bp in length
* 145939 145988: gap of 50 bp
* 145989 149971: contig of 3983 bp in length
* 149972 150021: gap of 50 bp
* 150022 154124: contig of 4103 bp in length
* 154125 154174: gap of 50 bp
* 154175 156468: contig of 2294 bp in length
* 156469 156790: gap of 322 bp
* 156791 171546: contig of 14756 bp in length
* 171547 171596: gap of 50 bp
* 171597 175250: contig of 3654 bp in length
* 175251 175301: gap of 50 bp
* 175302 190467: contig of 15167 bp in length
* 190468 190517: gap of 50 bp
* 190518 195552: contig of 5035 bp in length
* 195553 195602: gap of 50 bp
* 195603 198111: contig of 2509 bp in length
* 198112 199192: gap of 1281 bp
* 199193 202853: contig of 3461 bp in length
* 202854 202903: gap of 50 bp
* 202904 207061: contig of 4158 bp in length
* 207062 207111: gap of 50 bp
* 207112 212715: contig of 5604 bp in length
* 212716 212765: gap of 50 bp
* 212766 251666: contig of 38901 bp in length
* 251667 251716: gap of 50 bp
* 251717 258508: contig of 6792 bp in length
* 258509 259306: gap of 798 bp
* 259307 263777: contig of 4471 bp in length
* 263778 263901: gap of 124 bp
* 263902 275868: contig of 11967 bp in length
* 275869 277094: contig of 1126 bp in length
* 277095 277194: gap of unknown length
* 277195 278211: contig of 1017 bp in length
* 278212 278311: gap of unknown length
* 278312 279534: contig of 1223 bp in length
* 279535 279634: gap of unknown length
* 279635 280658: contig of 1024 bp in length
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* 280759 282222: contig of 1464 bp in length
* 282223 282322: gap of unknown length
* 282323 283471: contig of 1149 bp in length
* 283472 283571: gap of unknown length
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* 284999 285098: gap of unknown length
* 285099 286701: contig of 1603 bp in length
* 286702 286801: gap of unknown length
* 286802 288578: contig of 1777 bp in length
* 288579 288678: gap of unknown length
* 288679 290266: contig of 1588 bp in length

```

```

Query Match      63.0%; Score 25.2; DB 14; Length 303308;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 3 GATACCTACTCCCAACCAATCCATCTTACT 32
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Db 172671 GCTACCTACTCCCAACCAATACATATTACT 172700

```

```

RESULT 13
AC084290/c      linear      PRI 28-MAR-2002
LOCUS          Homo sapiens 12 BAC RP11-568G5 (Roswell Park Cancer Institute Human
DEFINITION     BAC Library) complete sequence.

```

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AC084290
AC084290.15 GI:19774277
HTG.
Homo sapiens (human)

REFERENCE AUTHORS

1 (bases 1 to 55001)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T., Barbiana, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carton, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyie, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, X., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, C., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kuchelapati, R., Weinstein, G., and Gibbs, R.

TITLE

Journal
Unpublished
2 (bases 1 to 55001)
Worley, K.C.

REFERENCE

Submitted (21-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE

Submitted (27-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE

Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Mar 28, 2002 this sequence version replaced gi:19747063.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email

gc-helpebcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
source	1..55001 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosomes="12" /clone="RP11-568G5"
misc_feature	1..1301 /note="overlaps bases 177088..178388 of clone AC079630"
repeat_region	35..229 /function="clone overlap" /rpt_family="L1P4"
repeat_region	1002..1023 /rpt_family="AT_rich"
repeat_region	1092..1227 /rpt_family="MIR"
repeat_region	complement(2156..2209) /rpt_family="L2"
repeat_region	3563..3650 /rpt_family="(CCGTA)n"
repeat_region	complement(3688..3765) /rpt_family="L2"
repeat_region	complement(3840..3908) /rpt_family="L1MD3"
repeat_region	complement(4234..4464) /rpt_family="MIR"
repeat_region	complement(4847..4914) /rpt_family="MIR"
repeat_region	4938..5053 /rpt_family="L2"
repeat_region	6350..6660 /rpt_family="AluSg"
repeat_region	complement(7309..7743) /rpt_family="LTR43"
repeat_region	7744..9144 /rpt_family="L1P4"

repeat_region	complement(9151..9317) /rpt_family="LTR43"
repeat_region	10587..10846 /rpt_family="L1M4"
repeat_region	10912..11015 /rpt_family="L1P"
repeat_region	11098..11271 /rpt_family="L1ME"
repeat_region	11450..11535 /rpt_family="MLTII"
repeat_region	11941..12179 /rpt_family="MIR"
repeat_region	12797..12828 /rpt_family="(CATATA)n"
repeat_region	complement(12975..13087) /rpt_family="FLAM_C"
repeat_region	13714..13737 /rpt_family="AT_rich"
repeat_region	14058..14219 /rpt_family="MER45"
repeat_region	14411..14545 /rpt_family="MIR"
repeat_region	complement(15058..15127) /rpt_family="MIR"
repeat_region	16185..16413 /rpt_family="MIR"
repeat_region	complement(17624..17922) /rpt_family="AluJb"
repeat_region	complement(18309..18606) /rpt_family="AluSx"
repeat_region	18844..18854 /rpt_family="AT_rich"
repeat_region	complement(18855..19135) /rpt_family="AluJb"
repeat_region	19136..19158 /rpt_family="AT_rich"
repeat_region	complement(20660..20753) /rpt_family="MER91C"
repeat_region	22179..22680 /rpt_family="(TAATA)n"
repeat_region	22180..22358 /rpt_family="AluJb"
repeat_region	22359..22632 /rpt_family="AluJb"
repeat_region	22833..22860 /rpt_family="(TAAAA)n"
repeat_region	22882..22789 /rpt_family="AluJb"
repeat_region	22796..23099 /rpt_family="AluY"
repeat_region	complement(23147..23327)

Query Match 60.0%; Score 24; DB 8; Length 55001;

Best Local Similarity 84.4%; Pred. No. 62;

Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATACTTACTCCCAACATCATCTTACTCAT 35

Db 47598 AACTTACTCCCAACATCATCTTACTCAT 47567

RESULT 14

AL807784/c	127196 bp	DNA	linear	ROD 13-NOV-2002
LOCUS	Mouse DNA	sequence from clone RP23-448C18 on chromosome X, complete		
DEFINITION	Mouse DNA	sequence.		
ACCESSION	AL807784			
VERSION	AL807784.11	GI:25045332		
KEYWORDS	HTG.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 127196)
Howden, P.
Direct Submission
Submitted (13-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 15, 2002 this sequence version replaced gi:24933941.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:

Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-448C18 is

from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6.

FEATURES

source

Location/Qualifiers
1. 127196
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-448C18"
/clone_lib="RPCI-23"

ORIGIN

Query Match 60.0%; Score 24; DB 9; Length 127196;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCAAACATCCATCTTACTATCATGCAAC 40
|||||
DB 110413 AGGATACATAGCAACCAATCACTTCTTACTAATGCCAC 110374
|||||

RESULT 15

AC157528

LOCUS

AC157528 154857 bp DNA linear PRI 27-APR-2005
Pan troglodytes BAC clone CH251-422M6 from chromosome unknown,
complete sequence.

DEFINITION

ACCESSION

AC157528

VERSION

AC157528.2

KEYWORDS

HTG.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Pan.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 154857)
Shah, N., Cotton, M. and Lewis, S.
The sequence of Pan troglodytes BAC clone CH251-422M6
Unpublished (2001)
2 (bases 1 to 154857)
Wilson, R.K.
Direct Submission
Submitted (18-FEB-2005) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 154857)
Wilson, R.K.
Direct Submission
Submitted (30-MAR-2005) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 154857)
Wilson, R.K.
Direct Submission
Submitted (27-APR-2005) Washington University School of Medicine,
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
63108, USA
On Mar 30, 2005 this sequence version, replaced gi:59933404.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: submissions@wustl.edu

----- Summary Statistics

Center project name: C_AB0422M06

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
<http://genome.wustl.edu>

SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the
Children's Hospital Oakland Research Institute, BACPAC Resources,
by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained
from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0471;
birthdate: 6-6-80). The clone and detailed information can be
obtained from Pieter de Jong and co-workers at
<http://www.bacpac.chori.org>.

This sequence is the entire insert of the clone.

FEATURES

source

Location/Qualifiers

1. 154857
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="unknown"
/clone="CH251-422M6"
/clone_lib="CHORI251"
74900
/note="Unresolved bases"
74903
/note="Unresolved bases"
127657..127881
/note="Sequence derived from one plasmid subclone."

unsure

unsure

unsure

ORIGIN

Query Match

60.0%; Score 24; DB 8; Length 154857;

Best Local Similarity 84.4%; Pred. No. 53;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATACCTACTCCAAACATCCATCTTACTCAT 35
| | | | | | | | | | | | | | | | | | | | |
Db 123632 AACTTACTCCAAACATCTTACTCAT 123663

Search completed: March 5, 2006, 21:55:41
Job time : 179.689 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 17:08:23 ; Search time 26.619 Seconds
(without alignments)
10014.946 Million cell updates/sec

Title: US-10-713-381-1_COPY_1239_1278

Perfect score: 40
Sequence: 1 aggatactactcccaaacatccatcttactatgcaac 40

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Geneseq 21.*
- 2: Geneseq 1980s.*
- 3: Geneseq 1990s.*
- 4: Geneseq 2000s.*
- 5: Geneseq 2001as.*
- 6: Geneseq 2002as.*
- 7: Geneseq 2002bs.*
- 8: Geneseq 2003as.*
- 9: Geneseq 2003bs.*
- 10: Geneseq 2003cs.*
- 11: Geneseq 2003ds.*
- 12: Geneseq 2004as.*
- 13: Geneseq 2004bs.*
- 14: Geneseq 2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	40	5	AAH76337
2	40	100.0	50	5	AAH76336 Z. mays M
3	40	100.0	158	5	AAH76334 Z. mays M
4	40	100.0	255	5	AAH76340 Z. mays M
5	40	100.0	1394	2	AAH76340 Z. mays M
6	40	100.0	1394	2	AAH76340 Z. mays M
7	40	100.0	1394	5	AAH76332 Z. mays M
8	40	100.0	1394	5	AAH76332 Z. mays M
9	30.4	76.0	2000	11	AAH76333 Z. mays M
10	22.4	56.0	226215	11	AAH76333 Z. mays M
11	21.6	54.0	4110	8	AAH76333 Z. mays M
12	21.6	54.0	6309	6	AAH76333 Z. mays M
13	21.6	54.0	7110	10	AAH76333 Z. mays M
14	21.6	54.0	7110	10	AAH76333 Z. mays M
15	21.6	54.0	7110	13	AAH76333 Z. mays M
16	21.6	54.0	7110	13	AAH76333 Z. mays M
17	21.4	53.5	1341	6	AAH76333 Z. mays M
18	21.4	53.5	6681	6	AAH76333 Z. mays M
19	21.4	53.5	6681	6	AAH76333 Z. mays M

C 20	21.4	53.5	8168	6	AAH76337
C 21	21.4	53.5	24401	4	AAH76337
C 22	21	52.5	1531	14	AAH76337
C 23	21	52.5	2000	11	AAH76337
C 24	21	52.5	2000	11	AAH76337
C 25	21	52.5	2792	12	AAH76337
C 26	21	52.5	3117	12	AAH76337
C 27	21	52.5	5507	8	AAH76337
C 28	21	52.5	5507	8	AAH76337
C 29	21	52.5	8404	4	AAH76337
C 30	21	52.5	8404	4	AAH76337
C 31	21	52.5	8404	10	AAH76337
C 32	21	52.5	8404	10	AAH76337
C 33	21	52.5	8404	10	AAH76337
C 34	21	52.5	8404	10	AAH76337
C 35	21	52.5	8404	13	AAH76337
C 36	21	52.5	8404	13	AAH76337
C 37	21	52.5	10286	4	AAH76337
C 38	21	52.5	10286	6	AAH76337
C 39	21	52.5	63115	10	AAH76337
C 40	21	52.5	63294	9	AAH76337
C 41	21	52.5	63294	10	AAH76337
C 42	21	52.5	63294	12	AAH76337
C 43	21	52.5	106315	11	AAH76337
C 44	20.8	52.0	891	8	AAH76337
C 45	20.8	52.0	6620	4	AAH76337

ALIGNMENTS

RESULT 1

AAH76337
ID AAH76337 standard; DNA; 40 BP.

AC AAH76337;

DT 29-OCT-2001 (first entry)

DE Z. mays Ms45 male tissue-preferred regulatory region fragment.

KW Ms45; male tissue; regulatory region; transcription; male fertility;

OS Zea mays.

PN WO200160997-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001MO-US004527.

PR 15-FEB-2000; 2000US-00504487.

XX (PION-) PIONEER HI-BRED INT INC.

XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;

XX WPI; 2001-514772/56.

XX A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the Ms45 gene useful for mediating fertility in a male plant.

XX Claim 14; Page 32; 50pp; English.

XX The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the Ms45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

CC present sequence represents a DNA fragment upstream of the TATA box of a
CC Z. mays Ms45 male-tissue preferred regulatory region nucleotide sequence
XX
SO Sequence 40 BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
Db 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||

RESULT 2
AAH76336
ID AAH76336 standard; DNA; 50 BP.
XX
AC AAH76336;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 male tissue-preferred regulatory region fragment.
XX
KW Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; ds.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US004527.
XX
PR 15-FEB-2000; 2000US-00504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garmaat CW, Huffman G, Kendall TL;
XX
DR WPI; 2001-514772/56.
XX
PT A male tissue-preferred regulatory region comprising nucleotide sequences
PT essential for initiating transcription of the MS45 gene useful for
PT mediating fertility in a male plant.
XX
PS Claim 5; Page 47; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the MS45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a DNA fragment -72 to -111 bases upstream of
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
CC nucleotide sequence
XX
SQ Sequence 50 BP; 18 A; 17 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
Db 11 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 50
|||||

RESULT 3
AAH76334

AAH76334 standard; DNA; 158 BP.
XX
AC AAH76334;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 male tissue-preferred regulatory region fragment.
XX
KW Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; ds.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US004527.
XX
PR 15-FEB-2000; 2000US-00504487.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Albertsen MC, Fox TW, Garmaat CW, Huffman G, Kendall TL;
XX
DR WPI; 2001-514772/56.
XX
PT A male tissue-preferred regulatory region comprising nucleotide sequences
PT essential for initiating transcription of the MS45 gene useful for
PT mediating fertility in a male plant.
XX
PS Claim 5; Page 47; 50pp; English.
XX
CC The invention provides a male tissue-preferred regulatory region (I)
CC comprising nucleotide sequences essential for initiating transcription of
CC the MS45 gene. A method of mediating male fertility in a plant is
CC provided that involves introducing an expression vector comprising a
CC promoter operably linked to (I) into a plant where the exogenous gene
CC impacts male fertility of the plant and (I) controls expression of the
CC exogenous gene. A method of producing hybrid seeds is also provided. The
CC present sequence represents a DNA fragment -38 to -195 bases upstream of
CC the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
CC nucleotide sequence
XX
SQ Sequence 158 BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 40; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
Db 86 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 125
|||||

RESULT 4
AAH76340
ID AAH76340 standard; DNA; 255 BP.
XX
AC AAH76340;
XX
DT 29-OCT-2001 (first entry)
XX
DE Z. mays Ms45 promoter fragment.
XX
KW Ms45; male tissue; regulatory region; transcription; male fertility;
KW hybrid seed; promoter; ds.
XX
OS Zea mays.
XX
PN WO200160997-A2.
XX
PD 23-AUG-2001.

XX PF 13-FEB-2001; 2001WO-US004527.
 XX PR 15-FEB-2000; 2000US-00504487.
 XX PA (PION-) PIONEER HI-BRED INT INC.
 XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 2001-514772/56.
 XX A male tissue-preferred regulatory region comprising nucleotide sequences
 PT essential for initiating transcription of the Ms45 gene useful for
 PT mediating fertility in a male plant.
 XX Example 5; Fig 8; 50pp; English.
 XX The invention provides a male tissue-preferred regulatory region (I)
 CC comprising nucleotide sequences essential for initiating transcription of
 CC the Ms45 gene. A method of mediating male fertility in a plant is
 CC provided that involves introducing an expression vector comprising a
 CC promoter operably linked to (I) into a plant where the exogenous gene
 CC impacts male fertility of the plant and (II) controls expression of the
 CC exogenous gene. A method of producing hybrid seeds is also provided. The
 CC present sequence represents a Z. mays Ms45 promoter fragment
 XX
 XX SQ Sequence 255 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 5; Length 255;
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
 DB 99 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 138
 RESULT 5
 AAX07408
 ID AAX07408 standard; DNA; 1394 BP.
 AC AAX07408;
 XX
 XX DT 08-JUN-1999 (first entry)
 XX Zea mays Ms45 male tissue-preferred regulatory region.
 XX Ms45; male; tissue-preferred; regulatory region; plant cells;
 XX Plant tissue; differentiated; maize; hybrid seed; fertility; ss.
 XX Zea mays.
 XX WO9859061-A1.
 XX 30-DEC-1998.
 XX 19-JUN-1998; 98WO-US012895.
 XX 23-JUN-1997; 97US-00880499.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 1999-105628/09.
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory
 CC region. It may be used in the construction of a vector for a method of
 CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, rolB and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating male fertile
 CC and infertile plants
 XX
 XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
 DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
 RESULT 6
 AAX07409
 ID AAX07409 standard; DNA; 1394 BP.
 AC AAX07409;
 XX
 XX DT 08-JUN-1999 (first entry)
 XX Zea mays Ms45 male tissue-preferred regulatory region.
 XX Ms45; male; tissue-preferred; regulatory region; plant cells;
 XX Plant tissue; differentiated; hybrid seed; fertility; ss.
 XX Zea mays.
 XX WO9859061-A1.
 XX 30-DEC-1998.
 XX 19-JUN-1998; 98WO-US012895.
 XX 23-JUN-1997; 97US-00880499.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 1999-105628/09.
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
 PT - useful in mediating plant fertility, especially hybrid seed production.
 XX
 XX Claim 3; Page 23-24; 39pp; English.
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory
 CC region. It may be used in the construction of a vector for a method of
 CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, rolB and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating male fertile
 CC and infertile plants
 XX
 XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
 DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, rolB and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating male fertile
 CC and infertile plants
 XX
 XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
 DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
 RESULT 6
 AAX07409
 ID AAX07409 standard; DNA; 1394 BP.
 AC AAX07409;
 XX
 XX DT 08-JUN-1999 (first entry)
 XX Zea mays Ms45 male tissue-preferred regulatory region.
 XX Ms45; male; tissue-preferred; regulatory region; plant cells;
 XX Plant tissue; differentiated; hybrid seed; fertility; ss.
 XX Zea mays.
 XX WO9859061-A1.
 XX 30-DEC-1998.
 XX 19-JUN-1998; 98WO-US012895.
 XX 23-JUN-1997; 97US-00880499.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
 XX WPI; 1999-105628/09.
 XX New nucleic acid encoding a Ms45 male tissue-preferred regulatory region
 PT - useful in mediating plant fertility, especially hybrid seed production.
 XX
 XX Claim 3; Page 23-24; 39pp; English.
 XX The sequence is that encoding an Ms45 male tissue-preferred regulatory
 CC region. It may be used in the construction of a vector for a method of
 CC producing exogenous genes in a male tissue-preferred manner, which is
 CC useful in restoring or conferring fertility, such as in hybrid seed
 CC production. In conferring fertility, a monocot/dicot plant is transformed
 CC with the exogenous nucleotide sequence (a male sterility gene, preferably
 CC Ms45), which encodes a product selected from auxins, rolB and diptheria
 CC toxin. Hybrid seeds are produced by cross-pollinating male fertile
 CC and infertile plants
 XX
 XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
 Query Match 100.0%; Score 40; DB 2; Length 1394;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
 DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

```

RESULT 7
AAH76332
ID AAH76332 standard; DNA; 1394 BP.
XX
XX AAH76332;
XX AC
XX
XX
XX 29-OCT-2001 (first entry)
XX
XX DE
XX Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX KW hybrid seed; ds.
XX KW
XX OS Zea mays.
XX
XX PN WO200160997-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX WPI; 2001-514772/56.
XX
XX DR
XX A male tissue-preferred regulatory region comprising nucleotide sequences
XX PT essential for initiating transcription of the Ms45 gene useful for
XX PT mediating fertility in a male plant.
XX
XX PS Claim 4; Page 46; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX CC comprising nucleotide sequences essential for initiating transcription of
XX CC the Ms45 gene. A method of mediating male fertility in a plant is
XX CC provided that involves introducing an expression vector comprising a
XX CC promoter operably linked to (I) into a plant where the exogenous gene
XX CC impacts male fertility of the plant and (I) controls expression of the
XX CC exogenous gene. A method of producing hybrid seeds is also provided. The
XX CC present sequence represents a nucleic acid sequence encoding an Ms45 male
XX CC -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 40; DB 5; Length 1394;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-06;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
XX |||||||
XX DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
XX
XX RESULT 8
XX AAH76333
XX ID AAH76333 standard; DNA; 1394 BP.
XX
XX AC AAH76333;
XX
XX XX
XX 29-OCT-2001 (first entry)
XX
XX DE
XX Z. mays Ms45 male tissue-preferred regulatory region encoding DNA.
XX
XX Ms45; male tissue; regulatory region; transcription; male fertility;
XX KW hybrid seed; ds.
XX KW
XX OS Zea mays.
XX
XX PN WO200160997-A2.

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XX
XX PD 23-AUG-2001.
XX
XX PF 13-FEB-2001; 2001WO-US004527.
XX
XX PR 15-FEB-2000; 2000US-00504487.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;
XX WPI; 2001-514772/56.
XX
XX DR
XX A male tissue-preferred regulatory region comprising nucleotide sequences
XX PT essential for initiating transcription of the Ms45 gene useful for
XX PT mediating fertility in a male plant.
XX
XX PS Claim 4; Page 47; 50pp; English.
XX
XX CC The invention provides a male tissue-preferred regulatory region (I)
XX CC comprising nucleotide sequences essential for initiating transcription of
XX CC the Ms45 gene. A method of mediating male fertility in a plant is
XX CC provided that involves introducing an expression vector comprising a
XX CC promoter operably linked to (I) into a plant where the exogenous gene
XX CC impacts male fertility of the plant and (I) controls expression of the
XX CC exogenous gene. A method of producing hybrid seeds is also provided. The
XX CC present sequence represents a nucleic acid sequence encoding an Ms45 male
XX CC -tissue preferred regulatory region from Z. mays
XX
XX SQ Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 40; DB 5; Length 1394;
XX Best Local Similarity 100.0%; Pred. No. 6.8e-06;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
XX |||||||
XX DB 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278
XX
XX RESULT 9
XX ACL38730
XX ID ACL38730 standard; cDNA; 2000 BP.
XX
XX AC ACL38730;
XX
XX XX
XX 02-JUN-2005 (first entry)
XX
XX DE Rice stress-regulated promoter SEQ ID NO:17293.
XX
XX KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX KW agriculture.
XX
XX OS Oryza sativa.
XX
XX PN WO2003008540-A2.
XX
XX PD 30-JAN-2003.
XX
XX PF 21-JUN-2002; 2002WO-US019668.
XX
XX PR 22-JUN-2001; 2001US-0300112P.
XX PR 24-AUG-2001; 2001US-0314662P.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 21-NOV-2001; 2001US-0332132P.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
XX PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX

```


PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.

XX Claim 48; SEQ ID NO 17293; 89pp; English.

XX The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

XX Sequence 2000 BP; 616 A; 370 C; 355 G; 659 T; 0 U; 0 Other;

Query Match 76.0%; Score 30.4; DB 11; Length 2000;
 Best Local Similarity 85.0%; Pred. No. 0.047;
 Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
 DB 1840 AGAACACCTACTCCCAACATCCATCGTCTACTCATGCAAC 1879

RESULT 10

ID ACN45146 standard; DNA; 226215 BP.

XX ACN45146;

DT 18-NOV-2004 (first entry)

XX Human genomic sequence HCG1639824.

XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

XX Homo sapiens.

XX WO2003073826-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006235.

XX 01-MAR-2002; 2002US-00087192.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 1948; 0pp; English.

XX The present invention relates to novel DNA and protein sequences which
 CC are associated with carcinomas. The sequences are useful for: (i) for
 CC screening drug candidates; (ii) for screening of bioactive agent capable
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;

CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
 CC carcinoma including lymphoma. The present sequence is one such CA coding
 CC sequence. Note: This patent is an equivalent to basic patent
 CC US2002182586A1, for which no sequence data was published

XX Sequence 226215 BP; 65331 A; 42804 C; 45218 G; 72862 T; 0 U; 0 Other;

Query Match 56.0%; Score 22.4; DB 11; Length 226215;

Best Local Similarity 72.5%; Pred. No. 1.4e+02;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40

DB 183206 AGAATTCCTGCTCCAAACACACGATCTTACTCCTTTTAC 183245

RESULT 11

ID ABZ10202/c

XX ABZ10202 standard; DNA; 4110 BP.

XX ABZ10202;

XX 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related DNA sequence #342.

XX Human; haematopoietic cell proliferation disorder; cytostatic;

KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KW cytosine methylation state; gene; ds.

XX Homo sapiens.

XX WO200277272-A2.

XX 03-OCT-2002.

XX 26-MAR-2002; 2002WO-EP003401.

XX 26-MAR-2001; 2001US-0278333P.

XX (EPIG-) EPIGENOMICS AG.

XX Berlin K.; Braun A.; Distler J.; Guetig D.; Howe A.; Mueller J.;

PI Olek A.; Piepenbrock C.; Adorjan P.; Grabs G.; Lesche R.; Leu E.;

PI Lewin A.; Lippecher E.; Maier S.; Model F.; Mueller V.; Otto T.; Pelet C.;

PI Schwope I.; Ziebarth H.;

XX WPI; 2003-018942/01.

XX Detecting and differentiating between hematopoietic cell proliferative

PT disorders, comprises contacting a target nucleic acid with a reagent that

PT distinguishes between methylated and non-methylated CpG dinucleotides.

XX Claim 28; SEQ ID NO 342; 117pp; English.

XX The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC lymphocytic leukaemia cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia, as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA

CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients

XX SQ Sequence 4110 BP; 945 A; 0 C; 1132 G; 2033 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 8; Length 4110;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACCAATCCATCTTAC 31
 Db 3083 AACCTAACCCCAACCAATCCATCTTAC 3056

RESULT 12

ABL32304/C
 ID ABL32304 standard; DNA; 6309 BP.

XX AC ABL32304;

XX DT 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 277.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianemic; cytostatic; neutropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antarthritic; antidiabetic; antipeoriatic;
 KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 XX ds.

XX OS Homo sapiens.

XX FN WO200200928-A2.

XX PD 03-JAN-2002.

XX PF 02-JUL-2001; 2001WO-EP007537.

XX PR 30-JUN-2000; 2000DE-01032529.

XX PR 01-SEP-2000; 2000DE-01043826.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.

XX PS Claim 1; SEQ ID NO 277; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention

XX SQ Sequence 6309 BP; 1758 A; 69 C; 1364 G; 3118 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 6; Length 6309;

Best Local Similarity 75.0%; Pred. No. 1.7e+02;

Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACCAATCCATCTTAC 39
 Db 3335 ATACTTATTCCCATAGACCAATCTCAATAATCCAA 3300

RESULT 13

ADB54282/C
 ID ADB54282 standard; DNA; 7110 BP.

XX AC ADB54282;

XX DT 04-DEC-2003 (first entry)

XX DE Pretreated genomic DNA region 206.

XX colon cell proliferative disorder; non methylated CpG dinucleotide;
 KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
 XX Unidentified.

XX PN WO2003072821-A2.

XX PD 04-SEP-2003.

XX PF 27-FEB-2003; 2003WO-EP002035.

XX PR 27-FEB-2002; 2002EP-00004551.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
 XX Rujan T, Schmitt A;

XX DR WPI; 2003-731620/69.

XX Detecting and differentiating between colon cell proliferative disorders
 PT associated with a gene or its regulatory regions comprises contacting a
 PT target nucleic acid in a biological sample obtained from the subject with
 PT a reagent.

XX Claim 32; SEQ ID NO 338; 74pp; English.

XX The invention relates to a novel method for detecting and differentiating
 CC between colon cell proliferative disorders associated with at least one
 CC gene or its regulatory regions. The method comprises contacting a target
 CC nucleic acid in a biological sample obtained from the subject with at
 CC least one reagent or a series of reagents, where the reagent or series of
 CC reagents distinguishes between methylated and non methylated CpG
 CC dinucleotides within the target nucleic acid. The molecules of the
 CC invention demonstrate cytosine methylation activity whilst the method may useful
 CC for detecting and differentiating between colon cell proliferative
 CC disorders, including cancers such as colon adenoma and colon carcinoma.
 CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
 CC determining cytosine methylation state or single nucleotide
 CC polymorphisms. The current sequence is that of the pretreated genomic DNA
 CC region of the invention. This sequence is not shown within the
 CC specification but is taken from Wipoweb.

XX SQ Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;

Query Match 54.0%; Score 21.6; DB 10; Length 7110;

Best Local Similarity 85.7%; Pred. No. 1.7e+02;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACCAATCCATCTTAC 31

Db 3083 AACCTAACCCCAACCAATCCATCTTAC 3056

RESULT 14

ADEB4196/C

ID ADE84196 standard; DNA; 7110 BP.
XX ADE84196;
AC
XX
DT 29-JAN-2004 (first entry)
XX
DE Human lymphoid cell proliferative disorder gene derived DNA #132.
XX
XX ds; lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis.
XX
XX Homo sapiens.
XX
XX WO2003044226-A2.
XX
XX 30-MAY-2003.
XX
XX 25-NOV-2002; 2002WO-EP013265.
XX
XX 23-NOV-2001; 2001DE-01057491.
XX
XX 28-DEC-2001; 2001DE-01064501.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX WPI; 2003-457621/43.
XX
XX Detecting and differentiating between lymphoid cell proliferative
PT disorders comprising a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated CpG
PT dinucleotides.
XX
XX Claim 26; SEQ ID NO 192; 448pp; English.
XX
XX The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least
CC one gene and/or their regulatory regions in a subject by contacting a
CC target nucleic acid in a biological sample obtained from the subject with
CC at least one reagent or series of reagents that distinguish between
CC methylated and non-methylated CpG dinucleotides within the target nucleic
CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GP1b beta, MYO11, CDH3,
CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN2A, CDKN2B, FOS,
CC GSTP1, HTC-1, MGMT, MLH1, MDS, MYC, PTEB, RBL2, TGFBR2, TP73, CDKN1C,
CC GSK3beta, ESR1, ARAF1, BAK1, BAX or HOTA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC CpG dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting or a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents a nucleic acid of a pretreated genomic DNA derived from the
CC above mentioned genes.
XX
XX Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;
SQ

Query Match 54.0%; Score 21.6; DB 10; Length 7110;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ATACCTACTCCCAACATCCATCTTAC 31
DB 3083 AAACCTACCCCAACATCCATCTTAC 3056

RESULT 15
ADS9580/c
ID ADS9580 standard; DNA; 7110 BP.
XX
AC ADS9580;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:596.
XX
XX ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
KW
XX Unidentified.
XX
XX WO2004035803-A2.
XX
XX 29-APR-2004.
XX
XX 01-OCT-2003; 2003WO-EP010881.
XX
XX 01-OCT-2002; 2002DE-01045779.
XX
XX 07-JAN-2003; 2003DE-01000096.
XX
XX 17-APR-2003; 2003DE-01017955.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Poekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
XX Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX WPI; 2004-348468/32.
XX
XX Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
XX Disclosure; SEQ ID NO 596; 104pp; English.
XX
XX The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analyzing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterization, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
XX Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;
SQ

Query Match 54.0%; Score 21.6; DB 13; Length 7110;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ATACCTACTCCCAACATCCATCTTAC 31
DB 3083 AAACCTACCCCAACATCCATCTTAC 3056

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Job time : 28.619 secs

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GenCore version 5.1.7
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(without alignments)
9910.279 Million cell updates/sec

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Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsel:
10: gb_gsel2:
11: gb_gsel3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	100.0	915	10	CG224225
3	40	100.0	963	9	CC656933
4	35.2	88.0	702	10	CW324514
5	24.2	60.5	296	10	CW445575
6	23.8	59.5	528	8	H24137
7	23.6	59.0	375	9	B2705605
8	23.2	58.0	738	7	CO117589
9	23.2	58.0	783	11	CR181951
10	23.2	58.0	1018	10	CL109241
11	23.2	58.0	1253	6	CD495749
12	23	57.5	405	9	A2883408
13	23	57.5	662	7	CJ037346
14	23	57.5	790	7	CJ035837
15	23	57.5	798	2	BG506830
16	23	57.5	968	2	BF143726
17	22.8	57.0	771	3	BM406466
18	22.8	57.0	1044	8	DN570622
19	22.6	56.5	398	10	CW888409
20	22.6	56.5	410	1	AW257178
21	22.6	56.5	560	2	BE205271
22	22.6	56.5	624	11	CR843833

C 23	22.6	56.5	630	9	BZ173201
C 24	22.6	56.5	644	11	CR843905
C 25	22.6	56.5	664	9	AZ400686
C 26	22.6	56.5	691	1	AW687128
C 27	22.6	56.5	736	11	CR818130
C 28	22.6	56.5	1080	10	CL058859
C 29	22.4	56.0	298	2	BB264116
C 30	22.4	56.0	804	8	DT054853
C 31	22.4	56.0	940	7	CK864514
C 32	22.4	56.0	940	7	CK871857
C 33	22.4	56.0	951	7	CN317130
C 34	22.2	55.5	273	1	AI206216
C 35	22.2	55.5	346	1	AI698201
C 36	22.2	55.5	398	1	AI725064
C 37	22.2	55.5	417	1	AI467879
C 38	22.2	55.5	479	2	BF601210
C 39	22.2	55.5	491	1	AI382034
C 40	22.2	55.5	609	3	BM027586
C 41	22.2	55.5	727	7	CK949745
C 42	22.2	55.5	802	10	CG811817
C 43	22.2	55.5	874	10	CZ727957
C 44	22.2	55.5	940	10	CG383910
C 45	22.2	55.5	1090	10	CL084441

ALIGNMENTS

RESULT 1
CC656939/c
LOCUS
DEFINITION
CC656939 genomic survey sequence.
VERSION
CC656939.1 GI:32060231
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays

CC656939 687 bp DNA linear GSS 19-JUN-2003
OGMDQ20TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0554D15,
genomic survey sequence.
CC656939
CC656939.1 GI:32060231
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 687)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Remick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.,
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGMDQ20TM
Contact: Cathy Whitelaw

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. .687
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0554D15"
/note="Vector: pGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source

ORIGIN
Query Match 100.0%; Score 40; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

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|||||
337 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 298

RESULT 2
CG224225          915 bp  DNA  linear  GSS 22-AUG-2003
LOCUS              OGIAG08TV_ZM_0.7_1.5_KB_Zea mays genomic clone ZMMBMA0716B15,
DEFINITION         genomic survey sequence.
ACCESSION          CG224225
VERSION            CG224225
KEYWORDS           GSS.
SOURCE             Zea mays
ORGANISM           Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 915)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGIAG08TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
1. 915
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBMA0716B15"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
Query Match 100.0%; Score 40; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 618 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 657

RESULT 3
CG656933
LOCUS              OGWDDQ20TM_ZM_0.7_1.5_KB_Zea mays genomic clone ZMMBMA0554D15,
DEFINITION         genomic survey sequence.
ACCESSION          CG656933
VERSION            CG656933
KEYWORDS           GSS.
SOURCE             Zea mays
ORGANISM           Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 963)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGWDDQ20TV

FEATURES
source
Query Match 100.0%; Score 40; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 618 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 657

RESULT 4
CW324514
LOCUS              702 bp  DNA  linear  GSS 31-OCT-2004
DEFINITION         104819_11477203.148_35910_078 Sorghum bicolor genomic clone 11477203, genomic survey
sequence.
ACCESSION          CW324514
VERSION            CW324514
KEYWORDS           GSS.
SOURCE             Sorghum bicolor (sorghum)
ORGANISM           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 702)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korff,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martensen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 819 row: c column: 19
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 702.
Location/Qualifiers
1. 702
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone_lib="11477203"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,

FEATURES
source
Query Match 100.0%; Score 40; DB 9; Length 963;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 836 AGGATACCTACTCCCAACATCCATCTTACTCATGCAAC 875

RESULT 4
CW324514
LOCUS              702 bp  DNA  linear  GSS 31-OCT-2004
DEFINITION         104819_11477203.148_35910_078 Sorghum bicolor genomic clone 11477203, genomic survey
sequence.
ACCESSION          CW324514
VERSION            CW324514
KEYWORDS           GSS.
SOURCE             Sorghum bicolor (sorghum)
ORGANISM           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 702)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korff,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martensen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 819 row: c column: 19
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 702.
Location/Qualifiers
1. 702
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone_lib="11477203"
/notes="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,

```

end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN

Query Match 88.0%; Score 35.2; DB 10; Length 702;
Best Local Similarity 92.5%; Pred. No. 0.0034; 3; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAAC 40
|||||
DB 74 AGGACACTTACTCCCAACAAATCCATGTTACCCATGCAAC 113
|||||

RESULT 5
CW445575 296 bp DNA linear GSS 02-NOV-2004
LOCUS fbb001f170m160 Sorghum methylation filtered library (LibID: 104)
DEFINITION Sorghum bicolor genomic clone fbb001f170m16, genomic survey
sequence.

ACCESSION

CW445575

VERSION CW445575.1 GI:55193536

KEYWORDS GSS

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 296)

Bedell, J.A., Budman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddell, J.A. and
Martienssen, R.A.

Sorghum genome sequencing by methylation filtration

PLoS Biol. 3 (1); e13 (2005)

15660154

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: fbb001f170 row: m column: 16

Seq primer: k Reverse

Class: methylation filtered

High quality sequence stop: 296.

Location/Qualifiers

1..296

/organism="Sorghum bicolor"

/mol_type="genomic DNA"

/cultivar="ATx623"

/db_xref="taxon:4558"

/clone="fbb001f170m16"

/clone_lib="Sorghum methylation filtered library (LibID: 104)"

/notes="Organ: leaf; Vector: pBCSK(-); Site: 1; HincII; DNA prepared from purified nuclei was randomly sheared end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

Query Match 60.5%; Score 24.2; DB 10; Length 296;
Best Local Similarity 90.2%; Pred. No. 75;
Matches 37; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AGGATACCTACTCCCAACAAAT-CCATCTTACTCATGCAAC 40
|||||

DB 242 AGGACACTTACTCCCAACAAATCCATGTTACCCATGCAAC 282
|||||

RESULT 6
H24137 528 bp mRNA linear EST 06-JUL-1995
LOCUS Ym50g08.r1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:51939 5', mRNA sequence.

ACCESSION

H24137

VERSION H24137.1 GI:892832

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Suarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 528)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

Insert Size: 1161

High quality sequence stops: 349

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1161

Seq primer: M13RP1

High quality sequence stop: 349.

Location/Qualifiers

1..528

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:424875"

/db_xref="taxon:9606"

/clone="IMAGE:51939"

/sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares infant brain INIB"

/note="Organ: whole brain; Vector: Lfamid BA; Site: 1; Not

1; Site 2: Hind III; 1st strand cDNA was primed with a Not

1 - oligo(dT) primer [5'

AACTCGAGAAATTCGCGCCGAGAAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lfamid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 59.5%; Score 23.8; DB 8; Length 528;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 ATACTCTCTCCCAACAAATCCATCTTACTCATGCA 38
|||||

DB 346 AAATCTACTCTCAACATTTTCATCTATACATGCA 380
|||||

ORIGIN

Query Match 59.5%; Score 23.8; DB 8; Length 528;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 ATACTCTCTCCCAACAAATCCATCTTACTCATGCA 38
|||||

DB 346 AAATCTACTCTCAACATTTTCATCTATACATGCA 380
|||||

RESULT 7
BZ706605/c 375 bp DNA linear GSS 18-MAY-2003
LOCUS SM14681-G07 55.13.ab1 Spider Monkey genomic BAC library Ateles
DEFINITION Geoffroyi genomic, genomic survey sequence.
ACCESSION BZ706605

VERSION BZ706605.1 GI:30843142
 KEYWORDS GSS.
 SOURCE Ateles Geoffroyi (black-handed spider monkey)
 ORGANISM Ateles Geoffroyi
 Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
 1 (bases 1 to 375)
 Qian, Y., Jin, L. and Su, B.
 Construction and characterization of bacterial artificial chromosome library of black-handed spider monkey (*Ateles Geoffroyi*)
 JOURNAL Genome 47 (2), 239-245 (2004)
 PUBLISHED 15060576
 COMMENT Contact: Qian Y, Jin L, Su B.
 Center for Genome Information
 University of Cincinnati
 Kettering Lab, 3223 Eden Ave., Cincinnati, OH 45267-0056, USA
 Tel: 1-513-558-6678
 Fax: 1-513-558-4505
 Email: subnucmail.uc.edu
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1..375
 /organism="Ateles Geoffroyi"
 /mol_type="genomic DNA"
 /strain="black-handed spider monkey"
 /db_xref="taxon:9509"
 /sex="Male"
 /tissue_type="Skin"
 /cell_type="Fibroblast"
 /cell_line="AG05352"
 /dev_stage="3 DA"
 /clone_lib="Spider Monkey genomic BAC library"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Genomic DNA was partially digested with EcoRI. Vector, pBAC3.6, Recombinants were transformed into DH10B."

ORIGIN
 Query Match 59.0%; Score 23.6; DB 9; Length 375;
 Best Local Similarity 74.4%; Pred. No. 1.4e+02;
 Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 2 GGATCTACTCCCAACCAATCCATCTTACTCATGCAAC 40
 |||||
 Db 255 GGATATCTACTGTGAACCATACATATTTACTNAGCAAC 217
 |||||

RESULT 8
 COL17589
 LOCUS GR_EB01H15.r GR_Eb Gossypium raimondii cDNA clone GR_EB01H15 3',
 DEFINITION mRNA sequence.
 ACCESSION COL17589.1 GI:48816276
 VERSION COL17589
 KEYWORDS EST.
 SOURCE Gossypium raimondii
 ORGANISM Gossypium raimondii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 1 (bases 1 to 738)
 Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
 Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and
 Wing, R. A.
 Global assembly of Cotton ESTs
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 The University of Arizona
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259

Email: rwing@genome.arizona.edu
 Plate: 01 row: H column: 15.
 FEATURES
 source
 1..738
 /organism="Gossypium raimondii"
 /mol_type="mRNA"
 /db_xref="taxon:29730"
 /clone="GR_EB01H15"
 /tissue_type="floral"
 /dev_stage="3 to +3 DPA"
 /lab_host="DH10B"
 /clone_lib="GR_Eb"
 /note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
 EcoRV; library made by Invitrogen with RNA supplied by
 Wendle lab. Directional cloned into NotI-EV. Colonies
 plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
 Query Match 58.0%; Score 23.2; DB 7; Length 738;
 Best Local Similarity 77.8%; Pred. No. 2.2e+02;
 Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 Qy 4 ATACTACTCCCAACCAATCCATCTTACTCATGCAA 39
 |||||
 Db 224 ATACACACTCCCATACACGCAAGTGACTCATGCAA 259
 |||||

RESULT 9
 COL181951
 LOCUS Reverse strand read from insert in 5'HPRT insertion targeting and
 DEFINITION chromosome engineering clone MHPN361p21, genomic survey sequence.
 ACCESSION COL181951.1 GI:49960800
 VERSION GSS; genome survey sequence; MICER.
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 783)
 Adams, D. J., Biggs, P. J., Cox, A. V., Davies, R. M., van der Weyden, L.,
 Jonkers, J., Smith, J., Plumb, J., Taylor, R. G., Nishijima, I., Yu, Y.,
 Rogers, J. and Bradley, A.
 Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER
 FEATURES
 source
 1..783
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN361p21"
 /clone_lib="MHPN"

ORIGIN
 Query Match 58.0%; Score 23.2; DB 11; Length 783;
 Best Local Similarity 77.8%; Pred. No. 2.2e+02;
 Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 Qy 4 ATACTACTCCCAACCAATCCATCTTACTCATGCAA 39
 |||||
 Db 514 ATACTACTCTAGCCCAATGCATCTTACTTCAGAA 549
 |||||

RESULT 10
 CL109241/c
 LOCUS CL109241
 DEFINITION ISB1-51D14_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-51D14,
 genomic survey sequence.
 ACCESSION CL109241
 VERSION CL109241.1 GI:40602876
 KEYWORDS GSS.

SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 1018)
AUTHORS Kramitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 72
High quality sequence stop: 524.

FEATURES
source
1..1018
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
/clone_lib="ISB1-51014"
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"

ORIGIN
Query Match 58.0%; Score 23.2; DB 10; Length 1018;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 156 TACATCTCTCCATACATCCATTTTAATGAATAC 121
|||||

RESULT 11
CD495749 1253 bp mRNA linear EST 12-JUN-2003
LOCUS CD418-D05.yid-s SHGC-CDA Gasterosteus aculeatus cDNA clone
DEFINITION CD418-D05 3', mRNA sequence.
ACCESSION CD495749 GI:31422780
VERSION CD495749
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
REFERENCE 1 (bases 1 to 1253)
AUTHORS Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,
Schmutz, J. and Myers, R.M.
TITLE Expressed sequence tags from Gasterosteus aculeatus
JOURNAL Unpublished (2003)
COMMENT Contact: Kingsley, DM
HMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cngm.stanford.edu
Plate: 18
High quality sequence start: 15
High quality sequence stop: 667.

FEATURES
source
1..1253
Location/Qualifiers
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"

/db_xref="taxon:69293"
/clone="CDA18-D05"
/sex="mixed male and female"
/tissue_type="heads and internal organs combined"
/dev_stage="adult"
/clone_lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI
(5' adaptor); Site 2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-CDNA method
by Stratagene. First strand cDNA synthesis was primed with
a 50 bp linker primer containing an oligo dt sequence
preceded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoRI cohesive end. The finished cDNAs
were inserted into the ZAP express vector
unidirectionally in the sense orientation with respect to
the lacZ promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."

ORIGIN
Query Match 58.0%; Score 23.2; DB 6; Length 1253;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TACCTACTCCCAACATCCATCTTACTCATGCAAC 40
|||||
Db 1047 TACCTCTTCCCAACATCCATCTTACCACATCCCAAC 1082
|||||

RESULT 12
AZ883408 405 bp DNA linear GSS 05-MAR-2001
LOCUS RPCI-23-18912.TJ RPCI-23 Mus musculus genomic clone RPCI-23-18912,
DEFINITION genomic survey sequence.
ACCESSION AZ883408
VERSION AZ883408
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 405)
AUTHORS Zhao, S., Niernman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akin, B., B. Levins, M., McGann, S., Teegay, G., Geer, K., Krol, M., de
Jong, F., and Fraser, C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-23-18912.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
pages: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 189 row: L Column: 2
Seq primer: SP6
Class: BAC ends
Location/Qualifiers
1..405
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-18912"

```

/sex="Female"
/lab host="DH10B"
/clone_lib="RPCI-23"
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcORI; Site_2: EcORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match          57.5%; Score 23; DB 9; Length 405;
Best Local Similarity 74.4%; Pred. No. 2.4e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 182 AGGTAACAATAATCCCAACAACTGCTTCTTAGTCATGCAA 144

RESULT 13
CJ037346
LOCUS
DEFINITION
CJ037346 662 bp mRNA linear EST 22-OCT-2004
scrofa cDNA clone TES01G080111 5', mRNA sequence.
ACCESSION
VERSION CJ037346.1 GI:54561241
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 662)
Unishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
14681463
COMMENT
Contact: Hirohide Unishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
source
1..662
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="TES01G080111"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
testis"
ORIGIN
Query Match          57.5%; Score 23; DB 7; Length 662;
Best Local Similarity 74.4%; Pred. No. 2.6e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 182 AGGTAACAATAATCCCAACAACTGCTTCTTAGTCATGCAA 144

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611 AGGAACCTGACTCCCAACAACTAGTAAGTAATCTATCCAA 649
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RESULT 14
CJ035837
LOCUS
DEFINITION
CJ035837 790 bp mRNA linear EST 22-OCT-2004
scrofa cDNA clone TES01E060090 5', mRNA sequence.
ACCESSION
VERSION CJ035837.1 GI:54559732
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 790)
Unishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
14681463
COMMENT
Contact: Hirohide Unishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
source
1..790
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="TES01E060090"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
testis"
ORIGIN
Query Match          57.5%; Score 23; DB 7; Length 790;
Best Local Similarity 74.4%; Pred. No. 2.7e+02;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
Db 609 AGGAACCTGACTCCCAACAACTAGTAAGTAATCTATCCAA 647
|||||

RESULT 15
BG506830/c
LOCUS
DEFINITION
BG506830 798 bp mRNA linear EST 27-MAR-2001
mRNA sequence.
ACCESSION
VERSION BG506830.1 GI:13468347
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

```

Wed Mar 8 14:17:01 2006

REFERENCE 1 (bases 1 to 798)
 NIH-MGC <http://mgc.nci.nih.gov/>
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgap@small.nhlbi.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLC916 row: e column: 11
 High quality sequence stop: 2.
 Location/Qualifiers
 1. .798
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4071154"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.5%; Score 23; DB 2; Length 798;
 Best Local Similarity 83.9%; Pred. No. 2.7e+02;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 ACTCCCAACATCCATCTTACTGTCGAC 40
 |||||
 Db 222 ACTCCCAACGCGCTTCTTAGTCATGATC 192

Search completed: March 6, 2006, 01:57:48
 Job time : 191.843 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.
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(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

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Maximum Match 100%
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4: /cgm2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/1/ina/6 COMB.seq.*
6: /cgm2_6/ptodata/1/ina/PTUS COMB.seq.*
7: /cgm2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgm2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgm2_6/ptodata/1/ina/backfile1.seq.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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4	20.6	51.5	601	3	US-09-949-002-7791
5	20.6	51.5	1071	3	US-09-248-796A-5546
6	20.6	51.5	14882	3	US-09-949-002-782
7	20.6	51.5	42075	3	US-09-949-016-14995
8	20.4	51.0	601	3	US-09-949-016-65770
9	20.4	51.0	973	3	US-09-774-528-184
10	20.4	51.0	973	3	US-10-120-988-184
11	20.4	51.0	4201	3	US-08-945-056-4
12	20.4	51.0	51770	3	US-09-949-016-13668
13	20.4	51.0	84571	3	US-09-949-016-17420
14	20.4	51.0	126200	3	US-09-949-016-11824
15	20.4	51.0	126200	3	US-09-949-016-13193
16	20.2	50.5	5099	3	US-09-610-040-5
17	20.2	50.5	5099	3	US-10-267-763-5
18	20.2	50.0	601	3	US-09-949-016-88655
19	20.0	50.0	2615	3	US-09-620-312D-22
20	20.0	50.0	77586	3	US-09-949-016-13220
21	20.0	50.0	77586	3	US-09-949-016-13221
22	19.8	49.5	107	3	US-09-513-999C-19002
23	19.8	49.5	601	3	US-09-949-016-202698
24	19.8	49.5	1017	3	US-09-710-279-2867

C 25	19.8	49.5	1164	3	US-09-134-001C-2534
C 26	19.8	49.5	2046	3	US-09-248-796A-6906
C 27	19.8	49.5	2971	3	US-09-710-279-3449
C 28	19.8	49.5	9366	3	US-09-949-016-17437
C 29	19.8	49.5	74096	3	US-09-949-016-11785
C 30	19.8	49.5	74097	3	US-09-949-016-16239
C 31	19.8	49.5	265038	3	US-09-949-016-15779
C 32	19.6	49.0	189	3	US-09-540-236-1562
C 33	19.6	49.0	601	3	US-09-949-016-83110
C 34	19.6	49.0	601	3	US-09-949-016-83111
C 35	19.6	49.0	601	3	US-09-949-002-4265
C 36	19.6	49.0	964	3	US-09-775-398-26
C 37	19.6	49.0	4322	2	US-08-537-342-1
C 38	19.6	49.0	6330	3	US-09-949-016-15506
C 39	19.6	49.0	6886	3	US-09-596-002-29
C 40	19.6	49.0	75480	3	US-09-949-016-16090
C 41	19.6	49.0	80858	3	US-09-949-016-12659
C 42	19.6	49.0	80859	3	US-09-949-016-15715
C 43	19.6	49.0	89892	3	US-09-949-016-13667
C 44	19.6	49.0	107937	3	US-09-949-016-17192
C 45	19.6	49.0	140315	3	US-09-949-016-14141

ALIGNMENTS

RESULT 1
US-08-880-499-1
; Sequence 1, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Carl, Garnaat W.
; APPLICANT: Hufman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-1
Query Match 100.0%; Score 40; DB 3; Length 1394;

Best Local Similarity 100.0%; Pred. No. 6e-07; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
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Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 2

US-08-880-499-2
; Sequence 2, Application US/08880499
; Patent No. 6037523
; GENERAL INFORMATION:
; APPLICANT: Albertson, Marc C.
; APPLICANT: Fox, Tim W.
; APPLICANT: Carl, Garuaat W.
; APPLICANT: Huffman, Gary A.
; APPLICANT: Kendall, Timmy L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
; TITLE OF INVENTION: AND METHOD OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880.499
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0578
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-880-499-2

Query Match 100.0%; Score 40; DB 3; Length 1394;
Best Local Similarity 100.0%; Pred. No. 6e-07; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
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Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 3

US-09-949-002-7790/c
; Sequence 7790, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7790
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-7790

Query Match 51.5%; Score 20.6; DB 3; Length 601;
Best Local Similarity 74.3%; Pred. No. 51;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACAATCCATCTTACTCATGCA 38
|||||
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RESULT 4

US-09-949-002-7791/c
; Sequence 7791, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7791
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-7791

Query Match 51.5%; Score 20.6; DB 3; Length 601;
Best Local Similarity 74.3%; Pred. No. 51;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 4 ATACTTACTCCCAACAATCCATCTTACTCATGCA 38
|||||
Db 379 ATAAAAACAACCAATCAATCAATCAATCTTCTCATGCA 345

RESULT 5

US-09-248-796A-5546
; Sequence 5546, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5546
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5546

US-09-248-796A-5546
; Sequence 5546, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5546
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5546

Query Match 51.5%; Score 20.6; DB 3; Length 1071;
Best Local Similarity 74.3%; Pred. No. 57; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 ATACTACTCCCAACCAATCCATCTTACTCATGCA 38
DB 224 ATCCCACTCTCAACATGTCACACTTACTTATCA 258

RESULT 6
US-09-949-002-782/c
; Sequence 782, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000730
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 782
; LENGTH: 14882
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-782

Query Match 51.5%; Score 20.6; DB 3; Length 14882;
Best Local Similarity 74.3%; Pred. No. 99;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 ATACTACTCCCAACCAATCCATCTTACTCATGCA 38
DB 8503 ATAAACACCAATCAATCAATCTTCTCATGCA 8469

RESULT 7
US-09-949-016-14995/c
; Sequence 14995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14995
; LENGTH: 42075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14995

Query Match 51.5%; Score 20.6; DB 3; Length 42075;
Best Local Similarity 85.2%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATACTACTCCCAACCAATCCATCTTACTCATGCA 30
DB 31591 ATCTTACCCCAACCAATCCATCTTACTCATGCA 31565

RESULT 8
US-09-949-016-65770/c
; Sequence 65770, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65770
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-65770

Query Match 51.0%; Score 20.4; DB 3; Length 601;
Best Local Similarity 71.1%; Pred. No. 61;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 GGATCTACTCTCCCAACCAATCCATCTTACTCATGCA 39
DB 414 GGATCTCTGGCTCAAGCAATCTCTCTCTCAGGCA 377

RESULT 9
US-09-774-528-184
; Sequence 184, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chonghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Felyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: Pct FL_genes Version 2.0
; SEQ ID NO 184
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (231)..(749)
US-09-774-528-184

Query Match 51.0%; Score 20.4; DB 3; Length 973;
Best Local Similarity 71.1%; Pred. No. 68;

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATACCTACTCCCAACATCCATCTTACTCATGCAA 39
Db 626 GGAATCACTCCAAAGAAACCTCGAAACCATGCAA 663

RESULT 10

US-10-120-988-184

; Sequence 184, Application US/10120988

; Patent No. 6919193

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Ren, Feiyan

; APPLICANT: Wang, Dunrui

; APPLICANT: Dmanac, Radoje T.

; TITLE OF INVENTION: No. 6919193el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 802CON

; CURRENT APPLICATION NUMBER: US/10/120,988

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: 09/774,528

; PRIOR FILING DATE: 2001-01-30

; NUMBER OF SEQ ID NOS: 441

; SOFTWARE: pc_FL_genes Version 2.0

; SEQ ID NO 184

; LENGTH: 973

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (231)..(749)

US-10-120-988-184

Query Match 51.0%; Score 20.4; DB 3; Length 973;

Best Local Similarity 71.1%; Pred. No. 68;

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATACCTACTCCCAACATCCATCTTACTCATGCAA 39

Db 626 GGAATCACTCCAAAGAAACCTCGAAACCATGCAA 663

RESULT 11

US-08-945-056-4

; Sequence 4, Application US/08945056

; Patent No. 607994

; GENERAL INFORMATION:

; APPLICANT: Coupland, George M.

; APPLICANT: Futterill, Joanna J.

; TITLE OF INVENTION: Genetic control of flowering

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon & Vanderhye PC

; STREET: 8th Floor, 1100 No. 6077994th Glebe Road

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/945,056

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/02561

; FILING DATE: 01-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9422083.7

; FILING DATE: 02-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Ms Mary J Wilson

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 620-17

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4201 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Arabidopsis thaliana

; STRAIN: Landsberg erecta

; POSITION IN GENOME:

; MAP POSITION: chromosome 5

US-08-945-056-4

Query Match 51.0%; Score 20.4; DB 3; Length 4201;

Best Local Similarity 80.0%; Pred. No. 92;

Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GATACCTACTCCCAACATCCATCTTACT 32

Db 2631 GATACCAGCTCCACCACTCAAACTTACT 2660

RESULT 12

US-09-949-016-13668/c

; Sequence 13668, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13668

; LENGTH: 51770

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(51770)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13668

Query Match 51.0%; Score 20.4; DB 3; Length 51770;

Best Local Similarity 71.1%; Pred. No. 1.6e+02;

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATACCTACTCCCAACATCCATCTTACTCATGCAA 39

Db 9851 GGATTCCTGGCTCAAGCAATCTCTGCTCAGGCAA 9814

RESULT 13

US-09-949-016-17420

; Sequence 17420, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17420
 ; LENGTH: 84571
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)---(84571)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-17420

Query Match 51.0%; Score 20.4; DB 3; Length 84571;
 Best Local Similarity 71.1%; Pred. No. 1.9e+02;
 Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATCTACTCCCAACATCCATCTTACTCTATGCAA 39
 Db 24559 GGAATCACTCCAAAGAACCTTCAAAACCATGCAA 24596

RESULT 14

US-09-949-016-11824/c
 ; Sequence 11824, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11824
 ; LENGTH: 126200
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)---(126200)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-11824

Query Match 51.0%; Score 20.4; DB 3; Length 126200;
 Best Local Similarity 71.1%; Pred. No. 1.9e+02;
 Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATCTACTCCCAACATCCATCTTACTCTATGCAA 39
 Db 53133 GGAATCACTCCAAAGAACCTTCAAAATCATGCAA 53096

RESULT 15

US-09-949-016-13193/c
 ; Sequence 13193, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13193
 ; LENGTH: 126200
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)---(126200)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-13193

Query Match 51.0%; Score 20.4; DB 3; Length 126200;
 Best Local Similarity 71.1%; Pred. No. 1.9e+02;
 Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 GGATCTACTCCCAACATCCATCTTACTCTATGCAA 39
 Db 53133 GGAATCACTCCAAAGAACCTTCAAAATCATGCAA 53096

Search completed: March 5, 2006, 22:36:24
 Job time : 13.1834 secs

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Wed Mar 8 14:17:00 2006

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 23:29:31 ; Search time 57.5163 Seconds
(without alignments)
5750.985 Million cell updates/sec

Title: US-10-713-381-1_COPY_1239_1278
Perfect score: 40
Sequence: 1 aggtactctactcccaacatctctctctctgcaac 40

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	40	100.0	40	US-10-713-381-6	Sequence 6, Appli
2	40	100.0	50	US-10-713-381-5	Sequence 5, Appli
3	40	100.0	158	US-10-713-381-3	Sequence 3, Appli
4	40	100.0	255	US-10-713-381-9	Sequence 9, Appli
5	40	100.0	1394	US-10-713-381-1	Sequence 1, Appli
6	40	100.0	1394	US-10-713-381-2	Sequence 2, Appli
7	24	60.0	85779	US-10-713-381-6880	Sequence 6880, Ap
8	23.2	58.0	706	US-10-424-599-31006	Sequence 31006, A
9	23.2	57.5	636	US-09-925-065A-670302	Sequence 670302,
10	22.6	56.0	294	US-10-425-115-143168	Sequence 143168,
11	22.4	56.5	315	US-10-424-599-83179	Sequence 83179, A
12	22.4	56.0	226215	US-10-087-192-1948	Sequence 1948, Ap
13	22.2	55.5	611	US-09-925-065A-591011	Sequence 591011,
14	22.2	55.5	611	US-09-925-065A-591012	Sequence 591012,
15	22.2	55.5	611	US-09-925-065A-591013	Sequence 591013,
16	22.2	55.5	613	US-09-925-065A-253727	Sequence 253727,
17	22.2	55.0	628	US-09-925-065A-888321	Sequence 888321,
18	21.6	54.0	598	US-09-925-065A-393490	Sequence 393490,
19	21.6	54.0	4110	US-10-473-126-342	Sequence 342, App
20	21.6	54.0	6309	US-10-311-455-277	Sequence 277, App
21	21.4	53.5	560	US-09-925-065A-281837	Sequence 281837,
22	21.4	53.5	560	US-09-925-065A-281838	Sequence 281838,
23	21.4	53.5	620	US-09-925-065A-189248	Sequence 189248,

24	21.4	53.5	653	4	US-09-925-065A-63167	Sequence 63167, A
25	21.4	53.5	1341	3	US-09-938-842A-1555	Sequence 1555, Ap
26	21.4	53.5	1341	3	US-09-938-842A-1555	Sequence 1555, Ap
27	21.4	53.5	6681	6	US-10-311-455-128	Sequence 128, App
28	21.4	53.5	6681	6	US-10-240-452-4	Sequence 4, Appli
29	21.4	53.5	8168	6	US-10-311-455-901	Sequence 901, App
30	21.4	53.5	8168	7	US-10-240-454-23	Sequence 23, Appli
31	21.4	53.5	24401	10	US-11-097-143-2335	Sequence 2335, Ap
32	21.4	53.5	3673778	6	US-10-312-841-1	Sequence 1, Appli
33	21.4	53.5	3673778	6	US-10-312-841-2	Sequence 2, Appli
34	21.4	53.5	293	7	US-10-424-599-24043	Sequence 24043, A
35	21.4	53.5	617	4	US-09-925-065A-285326	Sequence 285326,
36	21.4	53.5	617	4	US-09-925-065A-285327	Sequence 285327,
37	21.4	53.5	617	4	US-09-925-065A-285328	Sequence 285328,
38	21.4	53.5	653	4	US-09-925-065A-937247	Sequence 937247,
39	21.4	53.5	931	7	US-10-424-599-20320	Sequence 20320, A
40	21.4	53.5	2000	7	US-10-260-238-2594	Sequence 2594, Ap
41	21.4	53.5	2792	7	US-10-041-018-361	Sequence 361, App
42	21.4	53.5	3117	7	US-10-041-018-362	Sequence 362, App
43	21.4	53.5	5507	8	US-10-473-126-198	Sequence 198, App
44	21.4	53.5	5507	8	US-10-473-126-344	Sequence 344, App
45	21.4	53.5	8404	6	US-10-311-455-1568	Sequence 1568, Ap

ALIGNMENTS

RESULT 1		US-10-713-381-6		US-10-713-381-5	
		; Sequence 6, Application US/10713381		; Sequence 5, Application US/10713381	
		; Publication No. US20040221331A1		; Publication No. US20040221331A1	
		; GENERAL INFORMATION:		; GENERAL INFORMATION:	
		; APPLICANT: ALBERTSEN, MARC C.		; APPLICANT: ALBERTSEN, MARC C.	
		; APPLICANT: FOX, TIMOTHY W.		; APPLICANT: FOX, TIMOTHY W.	
		; APPLICANT: GARNAT, CARL W.		; APPLICANT: GARNAT, CARL W.	
		; APPLICANT: HUFFMAN, GARY		; APPLICANT: HUFFMAN, GARY	
		; APPLICANT: KENDALL, TIMMY L.		; APPLICANT: KENDALL, TIMMY L.	
		; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF		; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF	
		; FILE REFERENCE: USING SAME		; FILE REFERENCE: USING SAME	
		; CURRENT APPLICATION NUMBER: US/10713381		; CURRENT APPLICATION NUMBER: US/10713381	
		; CURRENT FILING DATE: 2003-11-14		; CURRENT FILING DATE: 2003-11-14	
		; PRIOR APPLICATION NUMBER: 08/880,499		; PRIOR APPLICATION NUMBER: 08/880,499	
		; PRIOR FILING DATE: 1997-06-23		; PRIOR FILING DATE: 1997-06-23	
		; NUMBER OF SEQ ID NOS: 24		; NUMBER OF SEQ ID NOS: 24	
		; SOFTWARE: PatentIn Ver. 2.0		; SOFTWARE: PatentIn Ver. 2.0	
		; SEQ ID NO 6		; SEQ ID NO 6	
		; LENGTH: 40		; LENGTH: 40	
		; TYPE: DNA		; TYPE: DNA	
		; ORGANISM: Zea mays		; ORGANISM: Zea mays	
		US-10-713-381-6		US-10-713-381-5	
		Query Match 100.0%; Score 40; DB 8; Length 40;		Query Match 100.0%; Score 40; DB 8; Length 40;	
		Best Local Similarity 100.0%; Pred. No. 4e-06;		Best Local Similarity 100.0%; Pred. No. 4e-06;	
		Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		1 AGGATACCTCTCCCAACATCTCTCTCTCTGCAAC 40		1 AGGATACCTCTCCCAACATCTCTCTCTCTGCAAC 40	
DB		1 AGGATACCTCTCTCCCAACATCTCTCTCTCTGCAAC 40		1 AGGATACCTCTCTCCCAACATCTCTCTCTCTGCAAC 40	
RESULT 2		US-10-713-381-5		US-10-713-381-5	
		; Sequence 5, Application US/10713381		; Sequence 5, Application US/10713381	
		; Publication No. US20040221331A1		; Publication No. US20040221331A1	
		; GENERAL INFORMATION:		; GENERAL INFORMATION:	
		; APPLICANT: ALBERTSEN, MARC C.		; APPLICANT: ALBERTSEN, MARC C.	
		; APPLICANT: FOX, TIMOTHY W.		; APPLICANT: FOX, TIMOTHY W.	
		; APPLICANT: GARNAT, CARL W.		; APPLICANT: GARNAT, CARL W.	
		; APPLICANT: HUFFMAN, GARY		; APPLICANT: HUFFMAN, GARY	
		; APPLICANT: KENDALL, TIMMY L.		; APPLICANT: KENDALL, TIMMY L.	
		; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF		; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF	
		; FILE REFERENCE: USING SAME		; FILE REFERENCE: USING SAME	

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; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-5

Query Match      100.0%; Score 40; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
Db 11 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 50

RESULT 3
US-10-713-381-3
; Sequence 3, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3

Query Match      100.0%; Score 40; DB 8; Length 158;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
Db 86 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 125

RESULT 4
US-10-713-381-9
; Sequence 9, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9

Query Match      100.0%; Score 40; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
Db 99 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 138

RESULT 5
US-10-713-381-1
; Sequence 1, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-1

Query Match      100.0%; Score 40; DB 8; Length 1394;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40
Db 1239 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 1278

RESULT 6
US-10-713-381-2
; Sequence 2, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
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us-10-713-381-1_copy_1239_1278.rnpbm

Wed Mar 8 14:17:00 2006

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; ORGANISM: Zea mays
US-10-713-381-2
Query Match
Best Local Similarity 100.0%; Score 40; DB 8; Length 1394;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGATCTACTCCCAACATCCATCTTACTCATGCAAC 40
DB 1239 AGGATCTACTCCCAACATCCATCTTACTCATGCAAC 1278

RESULT 7
US-10-719-993-6880/c
; Sequence 6880, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6880
; LENGTH: 85779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(85779)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6880

Query Match
Best Local Similarity 60.0%; Score 24; DB 8; Length 85779;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATACTCTACTCCCAACATCCATCTTACTCAT 35
DB 16082 AAATCTACTCCCAACATCTTACTCATCTCAT 16051

RESULT 8
US-10-424-599-31006
; Sequence 31006, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 31006
; LENGTH: 706
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128002C.1
US-10-424-599-31006

Query Match
Best Local Similarity 77.8%; Score 23.2; DB 7; Length 706;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TACTCTACTCCCAACATCCATCTTACTCATGCAAC 40
DB 1239 AGGATCTACTCCCAACATCCATCTTACTCATGCAAC 1278

RESULT 9
US-09-925-065A-670302/c
; Sequence 670302, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David C.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670302
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-09-925-065A-670302

Query Match
Best Local Similarity 57.5%; Score 23; DB 4; Length 636;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AGGATCTACTCTCCCAACATCCATCTTACTCATGCAAC 39
DB 474 AGGAAACGGATTAAACAACTATCCACCTTTCTCAGCAAC 436

RESULT 10
US-10-425-115-143168
; Sequence 143168, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143168
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_62049C.1
US-10-425-115-143168

Query Match
Best Local Similarity 56.5%; Score 22.6; DB 8; Length 294;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATACTCTACTCCCAACATCCATCTTACTCAT 32
DB 226 ATACTCTCTCCATCATCTTACTCAT 254
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RESULT 11

US-10-424-599-83179

Sequence 83179, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 83179

LENGTH: 315

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_46127C.1

US-10-424-599-83179

Query Match 56.0%; Score 22.4; DB 7; Length 315;

Best Local Similarity 81.2%; Pred. No. 69;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 ATACTACTCCCAACAATCCATCTTACTCAT 35

DB 211 AAACGAAGTCTTAACAAATCCATCTTAATCCT 242

RESULT 12

US-10-087-192-1948

Sequence 1948, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: CANCER

FILE REFERENCE: 529452000122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR FILING DATE: US 09/747,377

PRIOR APPLICATION NUMBER: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1948

LENGTH: 226215

TYPE: DNA

ORGANISM: Homo sapiens

US-10-087-192-1948

Query Match 56.0%; Score 22.4; DB 5; Length 226215;

Best Local Similarity 72.5%; Pred. No. 2.5e+02;

Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACAATCCATCTTACTCATGCAAC 40

DB 183206 AGAATTCCTGCTTCCAAACACAGCATCTTACTCTTTTAC 183245

RESULT 13

US-09-925-065A-591011/c

Sequence 591011, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

US-10-713-381-1_copy_1239_1278.rnpbm

Wed Mar 8 14:17:00 2006

; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO 591013
 ; LENGTH: 611
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-925-065A-591013

Query Match 55.5%; Score 22.2; DB 4; Length 611;
 Best Local Similarity 88.9%; Pred. No. 94;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CCAAAACCAATCTTACTCTATCTCAGC 40
 Db 351 CCAAAACCAATCTTACTCTATCTCAGC 325

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Wed Mar 8 14:17:00 2006

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Run on: March 6, 2006, 01:58:03 ; Search time 41.7555 Seconds
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2100.307 Million cell updates/sec

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Perfect score: 40
Sequence: 1 aggatactactcccaaacatccatcttactatgcaac 40

Scoring table: IDENTITY_NUC
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Searched: 7218535 segs, 1096242582 residues
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Maximum Match 100%
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3: /csm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
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12: /csm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
13: /csm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	57.5	636	US-09-925-065A-670302	Sequence 670302, A
2	22.6	56.5	3242	US-10-750-185-58624	Sequence 58624, A
3	22.6	56.5	3242	US-10-750-623-57406	Sequence 57406, A
4	22.2	55.5	611	US-09-925-065A-591011	Sequence 591011, A
5	22.2	55.5	611	US-09-925-065A-591012	Sequence 591012, A
6	22.2	55.5	611	US-09-925-065A-591013	Sequence 591013, A
7	22.2	55.5	613	US-09-925-065A-253727	Sequence 253727, A
8	22	55.0	628	US-09-925-065A-888321	Sequence 888321, A
9	21.6	54.0	598	US-09-925-065A-393490	Sequence 393490, A
10	21.4	53.5	560	US-09-925-065A-281837	Sequence 281837, A
11	21.4	53.5	560	US-09-925-065A-281838	Sequence 281838, A
12	21.4	53.5	620	US-09-925-065A-189248	Sequence 189248, A
13	21.4	53.5	653	US-09-925-065A-63167	Sequence 63167, A
14	21	52.5	201	US-11-124-367A-24503	Sequence 24503, A
15	21	52.5	617	US-09-925-065A-285326	Sequence 285326, A
16	21	52.5	617	US-09-925-065A-285327	Sequence 285327, A
17	21	52.5	617	US-09-925-065A-285328	Sequence 285328, A
18	21	52.5	653	US-09-925-065A-937247	Sequence 937247, A
19	21	52.5	1718	US-10-750-185-58624	Sequence 58624, A
20	21	52.5	1718	US-10-750-623-57406	Sequence 57406, A

21	20.8	52.0	1109	8	US-10-750-185-49907	Sequence 49907, A
22	20.8	52.0	1109	8	US-10-750-623-49907	Sequence 49907, A
23	20.8	52.0	1217	8	US-10-750-185-57406	Sequence 57406, A
24	20.8	52.0	1217	8	US-10-750-623-57406	Sequence 57406, A
25	20.6	51.5	50	12	US-11-175-859-103341	Sequence 103341, A
26	20.6	51.5	569	6	US-09-925-065A-127036	Sequence 127036, A
27	20.6	51.5	586	6	US-09-925-065A-610819	Sequence 610819, A
28	20.6	51.5	586	6	US-09-925-065A-696032	Sequence 696032, A
29	20.6	51.5	664	6	US-09-925-065A-696033	Sequence 696033, A
30	20.6	51.5	664	6	US-09-925-065A-696033	Sequence 696033, A
31	20.4	51.0	201	8	US-10-995-561-70646	Sequence 70646, A
32	20.4	51.0	413	6	US-09-925-065A-360599	Sequence 360599, A
33	20.4	51.0	470	6	US-09-925-065A-951077	Sequence 951077, A
34	20.4	51.0	507	6	US-09-925-065A-589111	Sequence 589111, A
35	20.4	51.0	507	6	US-09-925-065A-589112	Sequence 589112, A
36	20.4	51.0	507	6	US-09-925-065A-589113	Sequence 589113, A
37	20.4	51.0	507	6	US-09-925-065A-589114	Sequence 589114, A
38	20.4	51.0	507	6	US-09-925-065A-166775	Sequence 166775, A
39	20.4	51.0	519	6	US-09-925-065A-241631	Sequence 241631, A
40	20.4	51.0	545	6	US-09-925-065A-785033	Sequence 785033, A
41	20.4	51.0	552	6	US-09-925-065A-659195	Sequence 659195, A
42	20.4	51.0	558	6	US-09-925-065A-104305	Sequence 104305, A
43	20.4	51.0	568	6	US-09-925-065A-573143	Sequence 573143, A
44	20.4	51.0	576	6	US-09-925-065A-575922	Sequence 575922, A
45	20.4	51.0	583	6	US-09-925-065A-575923	Sequence 575923, A

ALIGNMENTS

RESULT 1
US-09-925-065A-670302/c
Sequence 670302, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925.065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 670302
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-670302

Query Match 57.5%; Score 23; DB 6; Length 636;
Best Local Similarity 74.4%; Pred. No. 11;
Matches 29; Conservative 0; Indels 0; Gaps 0;

QY 1 AGGATACCTACTCCCAACATCCATCTTACTATGCAA 39
Db 474 AGGAACGGATTACCAACTATCCACCTTTCTCAAGCAA 436

RESULT 2
US-10-750-185-58624
Sequence 58624, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:

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; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58624
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Bovine 19866880685452
US-10-750-185-58624

Query Match      56.5%; Score 22.6; DB 8; Length 3242;
Best Local Similarity 75.7%; Pred. No. 23;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      4 ATACCTACTCCAAACAATCCATCTTACTCATGCAAC 40
Db      2052 ATACCACCTACCAACCAAGTCAAGCTTATTGATGCAAC 2088

RESULT 3
US-10-750-623-58624
; Sequence 58624, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58624
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Bovine 19866880685452
US-10-750-623-58624

Query Match      56.5%; Score 22.6; DB 8; Length 3242;
Best Local Similarity 75.7%; Pred. No. 23;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      4 ATACCTACTCCAAACAATCCATCTTACTCATGCAAC 40
Db      2052 ATACCACCTACCAACCAAGTCAAGCTTATTGATGCAAC 2088

RESULT 4
US-09-925-065A-591011/c
; Sequence 591011, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 591011
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591011

Query Match      55.5%; Score 22.2; DB 6; Length 611;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14 CCAACAATCCATCTTACTCATGCAAC 40
Db      351 CCAACAACCAACCTTACTCATGCAAC 325

RESULT 5
US-09-925-065A-591012/c
; Sequence 591012, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 591012
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591012

Query Match      55.5%; Score 22.2; DB 6; Length 611;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14 CCAACAATCCATCTTACTCATGCAAC 40
Db      351 CCAACAACCAACCTTACTCATGCAAC 325

RESULT 6
US-09-925-065A-591013/c
; Sequence 591013, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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Wed Mar 8 14:17:00 2006

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 591013
LENGTH: 611
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-591013

* Query Match
Best Local Similarity 55.5%; Score 22.2; DB 6; Length 611;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 CCAACAATCCATCTTACTCATGCAAC 40
Db 351 CCAACAACACCTTACTCATGCGC 325

RESULT 7
US-09-925-065A-253727
Sequence 253727, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 253727
LENGTH: 613
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-253727

Query Match
Best Local Similarity 55.5%; Score 22.2; DB 6; Length 613;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GGATCTCTCCCAACATCCATCTTACTCATGCA 38
Db 292 GGATCTCTCCCAACATCCATCTTACTCATGCA 328

RESULT 8
US-09-925-065A-888321/c

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Sequence 888321, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 888321
LENGTH: 628
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-888321

Query Match
Best Local Similarity 55.0%; Score 22; DB 6; Length 628;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 GGATCTCTCTCCCAACATCCATCTTACTCATGCA 39
Db 224 GGATCTCTCTCCCAACATCCATCTTACTCATGCA 187

RESULT 9
US-09-925-065A-393490/c
Sequence 393490, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 393490
LENGTH: 598
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-393490

Query Match
Best Local Similarity 54.0%; Score 21.6; DB 6; Length 598;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TACTCTCTCCCAACATCCATCTTACT 32
Db 228 TACTCTCTCTCAATCAATCTTACT 201

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RESULT 10
US-09-925-065A-281837
; Sequence 281837, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281837
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-281837

Query Match      53.5%; Score 21.4; DB 6; Length 560;
Best Local Similarity 71.8%; Pred. No. 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
|||||
Db 373 AGGAATCACTCCAAAGGAACCTCGAACCCATGCAA 411

RESULT 11
US-09-925-065A-281838
; Sequence 281838, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281838
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-281838

Query Match      53.5%; Score 21.4; DB 6; Length 560;
Best Local Similarity 71.8%; Pred. No. 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGGATACCTACTCCCAACAAATCCATCTTACTCATGCAA 39
|||||
Db 373 AGGAATCACTCCAAAGGAACCTCGAACCCATGCAA 411

RESULT 12
US-09-925-065A-189248/c
; Sequence 189248, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189248
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-189248

Query Match      53.5%; Score 21.4; DB 6; Length 620;
Best Local Similarity 75.8%; Pred. No. 47;
Matches 25; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AGGTACTACTCCCAACAAATCCATCTTACTC 33
|||||
Db 175 ATGATAMCTACTTCCTATCTATGCTCACTC 143

RESULT 13
US-09-925-065A-63167
; Sequence 63167, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63167
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-63167

Query Match      53.5%; Score 21.4; DB 6; Length 653;
Best Local Similarity 71.8%; Pred. No. 47;
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Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 4 ATACCTACTCCCAACCAATCCATCTTACTCATGCAAC 40
 DB 387 ATACCTACTCCCAACCAATCCATCCAGGTTTGTAGCAAC 423
 Search completed: March 6, 2006, 10:32:46
 Job time : 41.7555 secs

Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1 AGGATACCTACTCCCAACCAATCCATCTTACTCATGCA 39
 DB 186 AGGAAACCTACACCTGACATGTCAACTAACTACTGCA 224

RESULT 14
 US-11-124-367A-24503
 ; Sequence 24503, Application US/11124367A
 ; Publication No. US20060024700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CL001519.ORD
 ; CURRENT APPLICATION NUMBER: US/11/124,367A
 ; CURRENT FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,846
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/582,609
 ; PRIOR FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: US 60/599,554
 ; PRIOR FILING DATE: 2004-08-09
 ; NUMBER OF SEQ ID NOS: 34460
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24503
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-11-124-367A-24503
 Query Match 52.5%; Score 21; DB 12; Length 201;
 Best Local Similarity 73.0%; Pred. No. 52;
 Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3 GATACCTACTCCCAACCAATCCATCTTACTCATGCA 39
 DB 43 GATACCTGTCTCAAAAATACATATTAAACATTAAA 79

RESULT 15
 US-09-925-065A-285326
 ; Sequence 285326, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.115
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 285326
 ; LENGTH: 617
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-925-065A-285326
 Query Match 52.5%; Score 21; DB 6; Length 617;
 Best Local Similarity 73.0%; Pred. NO. 68;

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